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Acc44693 Vector pA

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004as:* geneseqn2004bs:* geneseqn2005s:* geneseqn2003cs:* geneseqn2003ds:*

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SUMMARIES

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Result		Query				
No.	Score	Match	Match Length DB	DB	ព	Description
1	7580	100.0	7580	17	ADL71829	Ad171829 Arabidops
7	1730	22.8	1746	12	ADL71846	Adl71846 Arabidops
3	1402.4	18.5	10078	9	ABQ73047	Abq73047 Tomato an
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9	1360	17.9	1361	m	AAA88401	Aaa88401 4X CaMV 3
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80	1062	14.0	1062	12	ADL71848	Adl71848 Arabidops
6	1058	14.0	1058	12	ADL71847	Adl71847 Arabidops
10	888	11.7	888	12	ADL71840	Ad171840 Arabidops
11	692	9.1	795	10	ADD30377	Add30377 Plant yie
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13	684	9.0	684	12	ADL71843	Ad171843 Arabidops
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c 15	617.2	8.1	4727	14	AEA40942	Aea40942 T-DNA reg
16	617.2	8.1	8428	80	ABT16592	Abt16592 Artificia
17	617.2	8.1	8428	10	ACC44694	Acc44694 Plasmid p
18	617.2	8.1	10122	œ	ABT16598	Abt16598 Artificia
19	617.2	8.1	10122	10	ACC44701	Acc44701 Plasmid p

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       AACATGCAAAAGAATATATAGATTTACCGTATCAGATTTTCATACAATTTTTATATATTTTT
                                   GATATTGCTCTTTGAAACAACTAAACTGTGGAATTACAAGCTAAGGCAATATATTAT
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The invention relates to a transgenic plant transformed by a Dof transcription factor, OBF (ocs binding factor) binding protein (OBP3). OBP3 is also known as SOB1. The transgenic plant cell and OBP3 nucleic acid and polypeptides are useful in producing transgenic plants with altered size and stature and with normal and healthy root growth. The present sequence is Arabidopsis thaliana OBP3 DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGAAGGTGTTGCTTTACAACTATGAATATGGGCTCATGAGATGTACACTACAGATAAGCG
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                                                      Other
                                                      Sequence 7580 BP; 2376 A; 1376 C; 1291 G; 2537 T; 0 U; 0
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Matches 7580; Conservative 0
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                                                                              TCTTGGAGTAGACGAGAGTGTCGTGCTCCACCATGTTGGGGATCCACTAGTTCTAGAGCG
TTACCCTTTGTTGAAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTGATAT
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QV 5753 TAACCCACGAGAATTATGCACCTAAATTCAGACTAATCCCCCAAATTCAGAAATTTATG 5912 BD 1321 TAACCCACGAGAATTATGCACCTAAATTCAGAATTTCAGAAATTTATG 1380 QV 5913 TATTTTTGCGATTTAATATTGCTATCAATCACAACCCCAACTAATTGAAAGA 5972 DD 1381 TATTTTGCGATTTAATATTGCTACCAACCCCAACTCCAACTCAATTGAAAAGA 1440 DD 1441 CAATGGAATGACTGAAACCATCCAAGTCCAACTCCAACTCAATGAAAAGA 5912 QV 5933 ACCAATAGACTACATGAATCCTCAAGTCCCAACTCTAAGAAAAAAAA	REBULT 3 AB073047 standard; DNA; 10078 BP. XX AC AB073047; XX AC AB073047; XX AC AB073047; XX Tomato anthocyanin 1 (ANT1) related plasmid pAG3202 SEQ ID NO:3. XX Tomato, ANT1; anthocyanin 1; Lycopersicon esculentum; plant; colour; XX YX GONES GON
181 GATTACAATTCAAGCAACACTGGATTAGTGGAAACTCAAATAAGCAACAA 175	1513 TGTTGGTTGGGGGGTGALTGGTGCTTGTCATGCGGGGTTATTGCTGGGGAGATCAAACC 780 1011 TGTTGGTTGGGGTGTACATTGGTGCTTGTCATGCGGGTTATTGCTGGGGAGATCAAACC 780 1011 ATGCGGCTATATCCAAAGGCTAATTTTGAGGTTCAAAGGAAAGGTATGGTTATAAAATTA 5272 1012 ATGCAGCTATATCCAAAGGCTAATTTTGAGGTCCAAAGGAAAGGTATGGTTATAAAATTA 840 1013 ATGCAGCTATATCCAAAGGCTAATTTTGAGGTCCAAAGGAAAGGTATGGTTAATAAAATTA 840 1014 ATGCAGCTATATCCAAAGATCTTCAAAGTGTGAAAAGGAATGGTTAATAAAATTA 840 1021 GATATTATGTTTTATAAAAGATCTTCAAAGTGTGAATAATTATGGTTGGCTTCTGGT 900 1021 GATATTATGTTTTATAAAAATTTGGTTGAAAATTATGGTTGGCTTCTGGT 900 1022 GATATTATGTTTTATTAGAATTTGGTCTTATAATATGGCTGATTAAAAATAATTA 1020 1023 GATATTATGTTTTATTAGAATTTGGTCTTATAATATGGCTGATTAAAAATAATTA 1020 1024 GATATTATGTTTTATTAGAATTTGGTCTTATAATATGGCTTAATAAAAATAATTA 1020 1025 GATATCTAAAGAGTTGATGTTGGAAACTTTTTTGGTGTTCATTGAATAATAAT 1020 1026 GATTCTAAAAATTTCTTGGAGGTTGATGTTATTTTTTTGGTTCATTGAATAATAAT 1020 1027 GAATTCTAAAAGATTGATGATGTTGGAAACTTTTTTTTTGTGTTCATTGAATAATATT 1020 1028 GAATCTAATGAATTGAAGTTGATGTTGGAAACTTTTTTTT

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The invention comprises a plant gene activation vector that contains a hairy-root induction gene and enhancer and/or promoter which can function
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                                                                   TCTTCTGAGACTGTATCTTTGATATTCTTGAGAGTAGACGAGAGTGTCGTGCTCCACCATG
                TGGAATCCGAGGAGGTTTCCCGATATTACCCTTTGTTGAAAAGTCTCAATAGCCCTCTGG
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which is responsible for many red and blue colours in plants. The polynucleotide is useful for modifying e.g. leaf colour, flower colour fruit colour in plants. The present sequence represents the plasmid pAG3202 which is used in an example from the present invention for the generation of plants with an ANTI phenotype by transformation with an activation tagging construct
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Best Local Similarity 99.9%; Pred. No. 1.3e-207;
Matches 1403; Conservative 0; Mismatches 1;
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                             Sequence 17511 BP; 4453 A; 4201 C; 4511 G; 4344 T; 0 U; 2 Other;
  in a plant. The vector of the invention is useful for analyzing gene. The present DNA sequence is claimed in the invention.
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                                              Score 1367.4; DB 14; Lengt
Pred. No. 3.4e-202;
0; Mismatches 1; Indels
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16246 16426 16186 .. 0 7316 7376 The invention comprises a plant gene activation vector that contains a hairy-root induction gene and enhancer and/or promoter which can function in a plant. The vector of the invention is useful for analyzing a plant gene. The present DNA sequence is claimed in the invention. activation vector-related DNA sequence pHR-AT-GFP - SEQ ID 14. Novel plant gene active vector comprising hairy-root induction gene, and enhancer and/or promoter that functions in plant, useful for activating plant gene forming hairy root. GATATTACCCTTTGTTGAAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTG TTTTCCACGATGTTCCTCGTGGGGGGGTCCATCTTTGGGACCACTGTCGGTGGGACACA TCTACTGTCCTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCCC rcracrercerrecardaagracagarageregecaarggaarecgaggggrireee GATATTACCCTTTGTTGAAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTG TCTTGAACGATAGCCTTTCCCTTTATCGCAATGATGGCATTTTGTAGAAGCCATCTTCCTTT TTGGGGATCTAGATATCACATCAATCCACTTGCTTTGAAGACGTGGTTGGAACGTCTTCT Sequence 18987 BP; 4871 A; 4609 C; 4863 G; 4642 T; 0 U; 2 Other; AIAITCITGAAGIAGACAGAGAGTGTCGTGCTCCACCATGITGGGGAICC 7545 дв. gene activation vector; genetic analysis; 5; SEQ ID NO 14; 54pp; Japanese.

Gaps Query Match
Best Local Similarity 99.9%; Pred. No. 3.4e-202;
Matches 1368; Conservative 0; Mismatches 1; Indels 0; G

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Qy 7257 TTTTCCACGATGTTCCTCGTGGGTGGGGCTCCATTTGGGACCACTGTGGTAGAGGCA 7316 Db 17901 TTTTCCACGATGTTCCTTGGGGTGCATCTTTGGGACCACTGTGGGAGGCA 17842 Qy 7317 TCTTGAACGATAGCCTTTCCTTTTGGCATTGTAGAAGCCATCTTTTTGTAGAAGCCATCTTTTTTTT	RESULT 6 AAA88401/c ID AAA88401 standard; DNA; 1361 BP. XX AC AAA88401; XX XX DT 09-JAN-2001 (first entry)	XX	repeat_unit enhancer enhancer		enhancer repeat_unit enhancer
1898 TGTTTCGGATCTAGATATCACATCAATCCACTTGCTTTGAAGACGTGGTTGGAACGTC	6477 TTGATATTCTTGGAGTAGACGAGAGTGTCGTGCTCCACCATGTTGGGGATCTAGATATCA 6536		AAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTGATATTCTTGGAGTAGACG AAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTGATATTCTTGGAGTAGACG AAAGTCTCCACCTCTGGTCTTCTGAGACTGTATCTTTGATATTCTTTGAGAGAGCGAGC	18261 GACGTGGTTGGAACGTCTTCTTTTCCACGATGTTCCTCGTGGGGGGCTCTTTTG 18202 6957 GGACCACTGGTAGAGGATCTTGAACGATGGCTTTTCTTTATCGCAATGATGGCAT 7016 18201 GGACCACTGTGGTAGAGGCATCTTGAACGATAGCCTTTTATCGCAATGATGGCAT 18142 7017 TTGTAGAAGCCATCTTCTTTCTACTGTCCTTTTCGATGAACGTGACGGCAA 7076 18141 TTGTAGAAGCCATCTTCCTTTTCTACTGTCCTTTTCGATGAACTGACGGGCAA 18082	

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The present sequence is that of a 4X cauliflower mosaic virus (CaMV) 35S enhancer sequence preferred for use in the method of the invention. It includes 4 repeats of 202 bp AluI-EcoRV fragments of the 35S enhancer, and an additional 7 bp repeated sequence, which does not appear in the 35S enhancer region of the native CaMV genome. This 4X CaMV 35S enhancer can be used in a method for identifying genes associated with a Gelement can be used in a method for identifying genes associated with a desired trait in a fruit-bearing plant. The method involves: transforming plant cells with an activation tagging vector comprising an element which into the plant genes as selecting transformed plant cells, regenerating catering plant genes, selecting transformed plant cells, regenerating catering plants and characterizing the contribution of which has been enhanced, and confirming the contribution of the modified expression of each identified gene to the desired trait. The modified septence of the desired trait may be increased resistance to the desired trait. The modified seed number, plants, insects, modified leaf number, leaf pigmentation and shape, modified leaf number. Leaf pigmentation of confirming second resistance to the desired trait. The desired trait may endified seed number, pattern or distribution of leaves and flowers, modified seed number, pattern or distribution of leaves and clowers, modified seed number, pattern or distribution of leaves and clowers, modified seed number, pattern or distribution of leaves and clowers, modified seed number, pattern or distribution of leaves and clowers, modified seem length between nodes, root mass or root development characteristics or increased drought, salt and antibiotic commission by what wariation at increased drought, salt and antibiotic commission by what wariation at the cycles are transformed, as
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/*tag= n
/note= "CaMV 35S enhancer AluI-EcoRV fragment"
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/note= "129 bp fragment of the CaMV sequence" 1011. .1017 /*tag= m //note= "additional 7 bp not associated .1354 1018. .1354
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                                                160 TACTGTCCTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCCCGA
                                                                                         TATTACCCTTTGTTGAAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTGAT
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                                                                                                                            Arabidopsis thaliana OBP3 antisense DNA #9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 40; SEQ ID NO 20; 53pp; English.
                                           ADL71848 standard; DNA; 1062 BP
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New transgenic plant cell, useful in producing plants with altered size and stature and with normal and healthy root growth.
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                                                                                                                                                                                                                                             TITITGLCTCCGACCAATGTTTCAAACTCGAATCCTTTCGTTAAAAGTTGTTTCTGCTTTA
               841 GTTTAAAGTTACTATGACTTTAATCTGAGTTATTTATCCATTTTTTGCAGCTTTGT
3765 TAAAAACCTTTTTTCTTGTCTTCTCCCAAGGGCTTATGTATAATGTTTTTCTTACAGGATT
                                                                              GITTAAAAGITACTAIGACITTAAICIGAGITAITTAICCAITTICTITIIGCAGCITTGI
                                                                                                                                                                  3945 IGAAAAACTATAATTAATCTGCAATTCTTGTCAAAGTAGTCACAATTTTTATCTATTTTC
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100.0%; Pred. No. 4.1e-128;
ative 0; Mismatches 0;
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Matches 888; Conservative
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14.0%; Score 1058; DB 12;
Best Local Similarity 100.0%; Pred. No. 2.1e-154;
Matches 1058; Conservative 0; Mismatches 0;
                                                                                                                                      Claim 39; SEQ ID NO 19; 53pp; English.
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        AGATGTGACTCAACCAATACTAAGTTCTGTTACTTCAATAACTATAGCCTTACTCAACCT
                                                 AGATGTGACTCAACCAATACTAAGTTCTGTTACTTCAATAACTATAGCCTTACTCAACCT
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The invention relates to a number of isolated Arabidopsis thaliana CDNA sequences and their encoded proteins which are especially transcription factor bothA's and proteins. The isolated or recombinant plant transcription factor polymucleotides and polypeptides are useful in producing transgenic plants with commercially valuable properties, i.e. modified or altered desirable traits as compared to a reference plant, such as an alteration in a plant growth characteristic, e.g. growth rate, germination rate of seeds, vigor of plants and seedlings, or leaf and flower senescence. Sequence information related to the polymucleotides and polypeptides can also be used in bioinformatic search methods. The transgenic plant is useful for growing a progeny plant from a parent plant. This sequence represents one of the CDNAs of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New plant transcription factor polynucleotides and polypeptides, useful in producing transgenic plants with commercially valuable properties, such as an alteration in a plant growth characteristic, e.g. growth rate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGCCATTTCTGCAAAACATGTCGTCGCTATTGGACACGTGGCGGTTCCTTGAGGAATGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4292 AGATGTGACTCAACCAATACTAAGTTCTGTTACTTCAATAACTATAGCCTTACTCAACCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 795 BP; 236 A; 180 C; 175 G; 204 T; 0 U; 0 Other;
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r TL, Creelman RA,
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Pred. No. 8.2e-98;
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                                                                                                                                                                                                                                                                                                                                    Jiang C, Reuber TL,
                                                                                                                                                                                                                                                   (MEND-) MENDEL BIOTECHNOLOGY INC
                                                                                                     09-AUG-2001; 2001US-0310847P.
19-NOV-2001; 2001US-0336049P.
11-DEC-2001; 2001US-0338692P.
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                                                       2002WO-US025805
                                                                                                                                                                                            14-JUN-2002; 2002US-00171468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 89.5
les 795; Conservative
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P-PSDB; ADD30378.
                                                                                                                                                                                                                                                                                                    Ratcliffe O,
Pilgrim ML, J
Broun PE;
                                                    09-AUG-2002;
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20-FEB-2003
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301 AACCCTAGCAAGTTTCATAGCTACGGTCAAATCCCGGAGTTTAATTCCAACTTGCCCATC

AACCCTAGCAAGTTTCATAGCTACGGTCAAATCCCGGAGTTTAATTCCAACTTGCCCATC

4532

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ds; transcription factor; transgenic plant; growth rate; senescence; seed germination rate; plant vigor; seedling vigor.

Plant yield-related polynucleotide clone G1906.

(first entry)

15-JAN-2004

4351

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4771
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                                                                                                                                                                                                                 4832 GGTGATTCTCAACAGAAGAGTAGTGATTATTCCAATCAGCTAATGTTTAAGCCCTTGATG 4891
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421 GGAACTCAAATAAGCAACATGATAAGTGGTATCTAGTTCTAGTGGGGGATCTTGGATGCA
                                                                                                                        481 TGGAGAATACCTCCATCACAACAAGCTCAGCAATTCCCTTTCTTGATCAACACTACCGGA
                                                                                                                                                                                                                                                                                     -----AGGCGGGGTTAGCGCCACGCAAACAAGAAATGTGAAGGCGGAAGAGAAT
                                                                                                                                                                                                                                                                                                                                         5012 AATATCAACATAAACTCAGGCAGGAACGAGGAATACACATCATGGGGAGGTAACAGTTCT
                                                                                                                                                                                                                                                                                                                                                                                                 AATATCAACATAAACTCAGGCAGGAACGAGGAATACACACATCATGGGGAGGTAACAGTTCT
                                                      GGAACTCAAATAAGCAACATGATAAGTGGTATGAGTTTCTAGTGGTGGTGGATCTTGGATGCA
                                                                                                          TGGAGAATACCTCCATCACAACAAGCTCAGCAATTCCCTTTCTTGATCAACACTACCGGA
                                                                                                                                                                                                                                                                      4892 GATTTTTCTTCAGGCGGGGTTAGCGCCACGCAACAAGAAATGTGAAGGCGGAAGAGAT
                                                                                                                                                                                                                                                                                                                           952 GATCAGGATCGGGGTAGGGATGGGGATGGAGTGAATAACTTATCAAGAAACTTTTTGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                 TGGACCGGTTTCACCTCCAACAACTCAACAGGCCATCTCTCATTCTAA 5119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plant transcription factor related polynucleotide #1741.
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RIECHMANN J L.
JIANG C.
HEARD J E.
HAAKE V.
CREELMAN R A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2004019927-A1
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The invention describes a transgenic plant comprising a recombinant polynucleotide of any one of more than 500 nucleotide sequences fully defined in the specification or its complement. The method of the complement of the complement. The method of the chancin can be used to produced a plant having altered traits such as: enhanced tolerance to abiotic stress; glyphosphate tolerance; hormone sensitivity; disease resistance; sugar sensing; early or late flowering; altered flower structure, change in stem bifurcations, altered branching pattern, reduced apical dominance; reduced trichome density; lack of trichomes; reduced ectopic trichome development; altered trichome of trichomes; reduced root prowth; increased root development; altered seed development; altered cell proliferation or cell differentiation; rapid development; altered cell proliferation or cell differentiation; rapid development; contensed plant size; leaf morphology; seed morphology; seed biochemistry; increase in root anthocyanins; increase in plant size; decreased plant size; leaf morphology; seed contoyanins, or alteration in light response or shade avoidance. The transgenic plant, polynucleotides and polypeptides are useful in bioinformatic search methods. This sequence represents a plant transcription factor related polynucleotide.
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                                                                                                                                                                                                                                                                                                      New transgenic plant comprising a recombinant polynucleotide of any one of more than 500 nucleotide sequences, useful in bioinformatic search methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 AGATGTGACTCAACCAATACTAAGTTCTGTTACTTCAATAACTATAGCCTTACTCAACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 caccarrrcracaaaacargrcarcacrarragacacacargracrarcaraagaaargrr
                                                                                                                                                                                                Broun PE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 CCTGTTGGAGGAGGCTTTAGGAGGAAGAAGAGAAGCAAATCCAGATCGAAATCTACGGTC
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89.5%; Pred. No. 8.2e-98;
tive 0; Mismatches 0; Indels 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 795 BP; 236 A; 180 C; 175 G; 204 T; 0 U; 0 Other;
                                                                                                                                                                               Haake V;
Keddie J
                                                                                                                                                                             Riechmann JL, Jiang C, Heard JE,
Ratcliffe O, Adam LJ, Reuber TL,
Dubell AN, Pineda O, Yu G;
                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 2767; 435pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 89.5
Matches 795; Conservative
ADAM L J.
REUBER T L.
REDDIE J.
BROUN P E.
PILGRIM M L.
DUBELL A N.
PINEDA O.
YU G.
                                                                                                                                                                                                                                                    WPI; 2004-132245/13.
P-PSDB; ADI44305.
                                                                                                                                                                               Sherman BK,
Creelman RA,
                                                                                                                                                                                                                  Pilgrim ML,
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                (ADAM/)
(REUB/)
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(first entry)
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                                                                                                                                                 Local Similarity
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09-MAY-1995
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                                                                  GGAACTCAAATAAGCAACATGATAAGTGGTATGAGTTCTAGTGGTGGGATCTTGGATGCA
                                                                                    GGAACTCAAATAAGCAACATGATAAGTGGTATGAGTTCTAGTGGTGGTGGTGGAGCA
                                                                                                                                  TGGAGAATACCTCCATCACAACAAGCTCAGCAATTCCCTTTCTTGATCAACACTACCGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana OBP3 antisense DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 15; 53pp; English.
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transcription factor, OBF (ocs binding factor) binding protein (OBP3). OBP3 is also known as SOB1. The transgenic plant cell and OBP3 nucleic acid and polypeptides are useful in producing transgenic plants with altered size and stature and with normal and healthy root growth. The present sequence is Arabidopsis thaliana OBP3 antisense DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGTACTTCATCACTTACTTCTCGCCCAAGTTACTCAAACCCTAGCAAGTTTCATAGCTAC
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                                                                                                                                                                                                                                                      GATTACAATTCAAGCAACACTGGATTAGATTTGGTGGAACTCAAATAAGCAACATGATA
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0
                                                                                                                                                        Length 684;
                                                                                                                     Sequence 684 BP; 212 A; 145 C; 149 G; 178 T; 0 U; 0 Other;
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                                                                                                                                                        9.0%; Score 684; DB 12;
100.0%; Pred. No. 1.4e-96;
iive 0; Mismatches 0;
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Production method of a large amount of biologically active interleukin-12 protein using plant cell suspension culture cheaply and safely.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    interleukin-12; transgenic plant; Nicotiana tabacum; T-DNA; pMYL28; ds.
                                          7224 ACTIGCITIGAAGACGIGGIIGGAACGICTICITITICCACGAIGTICCICGIGGGIGG
                                                                                                                                                                                                                 503 ATAGCCCTTTGGTCTTCTGAGACTGTATCTTTGATATTCTTGGAGTAGACGAGAGTGTCG
                                                                                                                           GGTCCATCTTTGGGACCACTGTCGGTAGAGGCATCTTGAACGATAGCCTTTCCTTTATCG
                                                                                                                                                                                                                                                                           CAATGATGGCATTTGTAGAAGCCATCTTCCTTTTCTACTGTCCTTTCGATGAAGTGACAG
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                    623 CAAFGATGGCATTTGTAGGTGCCACCTTCCFTTTTCTACTGTCCTTTTGATGAAGTGACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence shows the nucleotide sequence for the plasmid designated pH11406. The plasmid vector contains the gene for MCDV (maize chlorotic dwarf virus) coat protein 3 placed under control of tandem cauliflower modaic virus 35S promoters isolated from the 1841 strain of the virus, and a polyA signal sequence obtained from the potato proteinase inhibitor [I] (Pin II) gene that exhibits enhancer-like activity. The chimeric gene also includes a 79 bp sequence omega' from the 5' leader region of tobacco mosaic virus that functions as a translational enhancer; and a zea mays alcohol dehydrogenase 1, intron 1 fragment spanning nucleotides [19-67, trimmed to 557 bp with Bal 31 nuclease, which has been shown to function as an enhancer of gene expression in monocots. The DNA is used for imparting resistance to MCDV or viruses to which MCDV infection or resistance provides cross-resistance, including maize dwarf mosaic virus resistance protection for plants. MCDV has a single, long RNA core used to provide protection for plants. MCDV has a single, long RNA core used to provide protection for plants. MCDV has a single, long RNA core which is shown in AAQ74694. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding maize chlorotic dwarf virus proteins - used to provide plants with resistance to the virus and related viral infections.
                                                                                                                             119. .672
/*tag= a
/noce= "Zea mays alcohol dehydrogenase 1, intron
fragment"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 5033;
  resistance; maize plant;
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Best Local Similarity 95.1%; Pred. No. 8.5e-87;
Matches 653; Conservative 0; Mismatches 30,
                                                                                                         Location/Qualifiers
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resistance; viral infection of dwarf mosaic virus; MDMV; ds
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                                                                                                                                                                                                                                         WO9421796-A2
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                                                              Synthetic
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p40; (c) isolating calluses of the transgenic plant of step (b) to produce a plant cell line(KCTC 1021BP); and (d) suspension culturing the plant cell line(KCTC 1021BP) to express the biologically active interleukin-12, wherein the plant is Nicotiana tabacum; gelatin may be further added into the medium in step (d) for improving production of IL-12; and the IL-12 contains a signal peptide. The present sequence represents T-DNA region of pWKL28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GATGGCATTTGTAGAAGCCATCTTCCTTTTCTACTGTCCTTTCGATGAAGTGACAGATAG
                                                                                                                                                                                                                                                                 CTGGGCAATGGAATCCGAGGAGTTTCCCGATATTACCCTTTGTTGAAAAGTCTCAATAG
                                                                                                                                                                                                                   TTTTGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCCCGATATTACCC
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                                                                                               Sequence 4727 BP; 1218 A; 1135 C; 1191 G; 1183 T; 0 U; 0 Other;
                                                                                                                      DB 14; Length 4727;
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                                                                                                                                              33; Indels
                                                                                                                    Query Match

8.1%; Score 617.2; DB 1.
Best Local Similarity 93.6%; Pred. No. 3.3e-86;
Matches 659; Conservative 0; Mismatches 33.
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Search completed: December 30, 2005, 17:26:48 Job time : 2706 secs

November 2005

Published Applications Nucleic Acid and Published Applications Amino Acid database searches now generate two sets of results each. The Published Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published Applications produce two sets of results, with the extensions rnpbm (Published Applications NA Main) and rnpbm (Published Applications NA New). Searches run against Amino Acid Published Applications produce two sets of results, with the extensions raphm (Published Applications AA New).

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December 30, 2005, 17:26:56 ; Search time 470 Seconds (without alignments) 8454.579 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result No.	ult No.	Score	Query Match	Length	DB	QI	Description	_
Ö	-	617.2	8.1	11667	9	US-10-508-263-122	Sequence 1	122,
υ	7	381.2	5.0	612	7	US-11-038-981A-1	Sequence 1	l, A <u>E</u>
υ	رهم	379.2	5.0	1459	7	US-11-038-981A-23	Sequence 2	3,
υ	4	377.6	5.0	3469	7	US-11-192-801-23	Sequence 2	3, 7
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υ	9	376.2	5.0	1467	7	US-11-038-981A-21	Sequence 2	11, 1
υ	7	374.6	4.9	1467	7	US-11-038-981A-22	Sequence 2	22, 1
υ	80	373.6	4.9	524	7	US-11-038-981A-6	Sequence 6	5, A
υ	σ	367.2	4.8	4149	7	US-11-192-801-13	Sequence 1	13, 7
υ	10	303.6	4.0	835	9	US-10-391-414-10	Sequence 1	10
	11	118	1.6	1935	7	US-11-038-981A-26	Sequence 2	56, 1
υ	12	116.2	1.5	332	7	US-11-038-981A-5	Sequence 5	š, A <u>r</u>
υ	13	116.2	1.5	1273	7	US-11-038-981A-18	Sequence 1	18,
υ	14	116.2	1.5	1273	7	US-11-038-981A-20	Sequence 2	7,07
υ	15	116.2	1.5	1281	7	US-11-038-981A-19	Sequence 1	7 ,61
υ	16	116.2	1.5	1935	7	US-11-038-981A-25	Sequence 2	25, ;
υ	11	116.2	1.5	1939	7	US-11-038-981A-24	Sequence 2	24, 1
υ	18	116.2	1.5	1963	7	US-11-038-981A-27		27, 1
	19	116.2	1.5	1963	7	US-11-038-981A-28		28,
U	20	116.2	1.5	1971	7	US-11-038-981A-29		7 62
	21	101.6	1.3	986	9	US-10-927-641-40	Seguence 4	70,
	22	88.6	1.2	762	9	US-10-509-691-1	Sequence 1	l, A
O	23	78.2	1.0	173602	7	US-11-121-086-25		25,

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Sequence 105, App Sequence 25, Appl Sequence 29, Appl Sequence 29, Appl Sequence 13443, A Sequence 1343, A Sequence 13235, A Sequence 11, Appl Sequence 16, Appl Sequence 11, Appl Sequence 1314, A Sequence 1316, Appl Sequence 1316, Appl Sequence 1316, Appl Sequence 1316, Appl	Sequence 38, Appl Sequence 20, Appl Sequence 11, Appl Sequence 11, Appl Sequence 9, Appli Sequence 10, Appli Sequence 10, Appli
US-11-121-086-105 US-11-121-086-105 US-11-121-086-105 US-10-240-708-29 US-10-240-708-47 US-10-240-708-61 US-10-295-561-13433 US-10-995-561-13235 US-10-995-561-1314 US-11-038-981A-16 US-11-0395-561-1314 US-10-995-561-1314 US-10-995-561-1314	US-10-240-708-38 US-10-240-708-38 US-11-038-981A-2 US-11-038-981A-11 US-11-038-981A-10 US-11-038-981A-10 US-11-038-981A-4
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ALIGNMENTS

SULT 1 -10-508-263-263-122/c bublication No. US20050260754A1 SPUBLICATION No. US20050260754A1 GENERAL INFORMATION: APPLICANT: BASF Plant Science GmbH TIPLE OF INVENTION: Constructs and methods for regulating gene expression TIPLE OF INVENTION: Constructs and methods for regulating gene expression TIPLE OF INVENTION: CONSTRUCTS 3262-20085.00 CURRENT APPLICATION NUMBER: US/10/508,263 CURRENT FILING DATE: 2004-09-20 SOFTWARE: PSQ ID NOS: 126 SOFTWARE: PSQ ID NOS: 126 SOFTWARE: DNA ORGANISM: Artificial sequence FEATURE: CTYPE: DNA ORGANISM: Artificial sequence FEATURE: CTHER INFORMATION: CONSTRUCT 2 p3300.1-Toc159-GFP-RNAi -10-508-263-122	8.1%; Score 617.2; DB 6; Length 11667; .larity 93.6%; Pred. No. 1.4e-96; .Conservative 0; Mismatches 33; Indels 12; Gaps 1;	AGATATCACATCAATCCACTTGCTTTGAAGACGTGGTTGGAACGTCTTCTTTTTCCACGA 6927	TGTTCCTCGTGGGGTGGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCATCTTGAACGA 6987	TAGCCTTTCCTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCCTTTTCTACTGTCC 7047 	TITICGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGATTTCCCGATATTACCC 7107 	TITIGITGAAAAGICICAATAGCCCTCIGGICITCIGAGACIGIAICITTGATAITCTIGG 7167 	AGTAGACGAGAGTGTCGTGCTCCACCATGTTGGGGATCTAGATATCACATCAATCCACTT 7227
SULT 1 -10-508-263-122/c sequence 122, Application bublication No. US200502 GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: CURENT SAPPLICATION CONTRIBUTE OF INVENTION: FILE REFERENCE: 53262-2 CURRENT APPLICATION NUM CURRENT FILING DATE: 12 NUMBER OF SEQ ID NOS: 11 SOFTWARE: PatentIN Ver. SEQ ID NO 122 LENGTH: 11667 TYPE: DNA ORGANISM: Artificial su FRATURE: FRATURE: CTHER INFORMATION: CONTRER INFORMATION: CON-	겯	AGATATCACAT AGATATCACAT		TAGCCTTTCCT	TTTCGATGAAG TTTTGATGAAG	TTTGTTGAAAA TTTGTTGAAAA	
RESULT 1 US-10-508-263-122/c Sequence 122, App Publication No. U GENERAL INFORMATI APPLICANT: BASF TITLE OF INVENTI: TILE REPERENCE: CURRENT FILING D NUMBER OF SEQ ID SOFTWARE: Patent CURRENT FILING D NUMBER OF SEQ ID SOFTWARE: Patent CURRENT FILING TUPE: DNA OGGANISM: Artif FRATURE: COTHER INFORMATI US-10-508-263-122	al el	6868	6928	6988	7048	7108	7168
RESULT 1 US-10-506 Poducer Publicer GENERAL TITLE FILE FURREN CURREN CURREN NUMBER SEO ID SEO ID LENGT CRADE CURREN NUMBER SEO ID CRADE CURREN	Query Ma Best Loc Matches	දුරු	දු දු	کو م	& q	Oy Op	à

6490 AGTAGACGAGAGTGTCGTGCTCCACCATGTTGGGGATCTAGATATCACATCAATCCACTT 262CATCACATCAATCCACTT	Qy 6550 GCTTTGAAGACGTGGTTGGAACGTCTTCTTTTCCACGATGTTCCTCGTGGGTTGGGGTC 6600 All	Db 184 CATCTTTGGGACCACTGTCGGCAGAGCATCTTCAACGATGGCCTTTCCTTTATCGCAAT 125 Qy 6670 GATGGCATTTGTAGAAGCCATCTTCCTTTCTACTGTCCTTTCGATGAGGATAG 6729		Db 64 CTGGGAATGGAATCGAGGAGGTTTCCGGATATTACCCTTTGTTGAAAAGTCTCAATCG 5	NS-11-038-981A-23/c Sequence 23, Application US/11038981A Publication No. US20050283856A1	GENERAL INFORMATION: APPLICANT: Conner, Timothy W. APPLICANT: Flasinski, Stanislaw APPLICANT: Pang, Sheng Z APPLICANT: Pang, Ching Z TITLE OF INVENTION: CHIMBRIC PROMOTERS FOR USE IN PLANTS FILE REFERENCE: 38-21 (51446) B	CURRENT APPLICATION NUMBER: US/11/038,981A ; CURRENT FILING DATE: 2005-01-20 ; PRIOR APPLICATION NUMBER: 60/537,793 ; PRIOR FILING DATE: 2004-01-20	; NUMBER OF SEQ ID NOS: 35 ; SEQ ID NO 23 ; LENGTH: 1459 ; TYPE: DNA ; ORGANISM: Artificial Sequence		Query Match 5.0%; Score 379.2; DB 7; Length 1459; Best Local Similarity 80.4%; Pred. No. 3.6e-56; Matches 492; Conservative 0; Mismatches 43; Indels 77; Gaps 1;	Oy 6174 CTTTTGTTTCGGATCTAGATATCACATCAATCCACTTGCTTTGAAGACGTGGTTGGAACG 6233	Oy 6234 TCTTCTTTTCCACGATGTCCTCGTGGGGGGGCTCCATCTTTGGGACCACTGTCGGTA 6293	OY 6294 GAGGCATCTTGAACGATAGCCTTTCCTTTATCGCAATGATGACGAATTTGTAGAAGCCATCT 6353	OY 6354 TCCTTTCTACTGTCCTTTCGATGAGATAGCTGGGCAATGGAATCCGAGGGG 6413	Oy 6414 TITCCGATATTACCCTTTGTTGAAAAGTCTCAATAGCCCTCTGGGCTCTTCTGAGACTGTA 6473	Qy 6474 TCTTTGATATTCTTGGAGTAGACGAGAGTGTCGTGCTCCACCATGTTGGGGGATCTAGATA 6533
	Db 764 GCTTTGAAGACGTGGTTGGAACGTCTTCTTTTCCACGATGCTCGTGGTGGGGGTC 705	Qy • 7348 GATGGCATTTGTAGAAGCCATCTTTCTACTGTCCTTTCGATGAAGTGACAGATAG 7407	Oy (7408 CTGGGCAATGGAATCCGAGGGTTTCCCGATATTACCCTTTGTTGAAAGTCTCAATAG 7467 Db 584 CTGGGCAATGGAATCCGAGGGGTTTCCCGATATTACCCTTTGTTGAAAAGTCTCAATAG 525	Oy 7468 CCCTCTGGTCTTCTGAGACTGTATCTTTGATATTCTTGGAGTAGACGAGAGTGTCGTGCT 7527	Qy 7528 CCACCATGTTGGGGATCCACTAGTTCTAGAGGGCCGCCACGGC 7571	RESULT 2 US-11-038-981A-1/c ; Sequence 1, Application US/11038981A ; Publication No. US20050283856A1 ; ENUPAR INFORMATION	APPLICANT: Conner, Timothy W. APPLICANT: Flasinski, Stanislaw APPLICANT: Pang, Sheng Z APPLICANT: You, Jinsong	; TITLE OF INVENTION: CHIMMENIC PROMOTERS FOR USE IN PLANTS; FILE REFERENCE: 38-21(51446)B ; CURRENT APPLICATION NUMBER: US/11/038,981A ; CURRENT FILING DATE: 2005-01-20 ; PRIOR APPLICATION NUMBER: 60/537,793	03		Query Match 5.0%; Score 381.2; DB 7; Length 612; Best Local Similarity 81.5%; Pred. No. 1.2e-56; Matches 489; Conservative 0; Mismatches 33; Indels 78; Gaps 1;	QY 6190 AGATATCACATCAATCCACTTGCTTTGAAGACGTGGTTGGAACGTCTTCTTTTCCACGA 6249 DD 526 AGATATCACATCAATCACTTGCTTTGAAGACGTGGTTGGAACGTCTTTTTCCACGA 467	Oy 6250 TGTTCCTCGTGGGTGGGGGCTCCATCTTTGGGACCACTGTCGGTAGAGGCATCTTGAACGA 6309	Qy 6310 TAGCCTTTCCTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCCTTTTCTACTGTCC 6369 Db 406 TGGCCTTTCCTTTATCGCAATGATGGCATTTGTAGGAGCCACCTTCCTT	QY 6370 TTTCGATGAAGAGAGATAGCTGGGGAATGGAATCCGAGGAGGTTTCCCGATATTACCC 6429	Oy 6430 TITGITGAAAAGTCTCAAIAGCCCTCTGGTCTTCTGAGACTGTATCTTGATAITCTTGG 6489

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Sequence 15, Application US/11192801
| Publication No. US20050273882A1
| GENERAL INFORMATION:
| APPLICANT: Romano. Charles P. |
| APPLICANT: Romano. Charles P. |
| TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants |
| FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn |
| CURRENT APPLICATION NUMBER: US/11/192,801 |
| CURRENT PILING DATE: 2005-07-29 |
| PRIOR FILING DATE: 2002-08-29 |
| PRIOR FILING DATE: 1999-08-19 |
| PRIOR FILING DATE: 1999-08-19 |
| NUMBER OF SEQ ID NOS: 43 |
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553 AGATATCACATCAATCCACTTGCTTTGAAGACGTGGTTGGAACGTCTTCTTTTTCCACGA 494
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                                                                   493 TGCTCCTCGTGGGGGGTCCATCTTTGGACCACTGTCGGCAGAGGCATCTTCAACGA
                                                                                                                            6310 TAGCCTTTCCTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCCTTTTCTACTGTCC
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LOCATION: (25)..(640)
OTHER INFORMATION: P-CAMV.35S
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OTHER INFORMATION: I-Zm.Hsp70
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LOCATION: (1490)..(3448)
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US-11-192-801-15/c
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LENGTH: 37
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Sequence 23, Application US/11192801

Fublication No. US20050273882A1

GENERAL INFORMATION:

APPLICANT: Romano.

TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants

FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn

CURRENT APPLICATION NUMBER: US/11/192,801

CURRENT PILING DATE: 2005-07-29

PRIOR PILING DATE: 2005-07-29

PRIOR APPLICATION NUMBER: US/09/377,466

PRIOR PILING DATE: 1999-08-19

NUMBER OF SEQ ID NOS: 43

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO S: 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: CDS
LOCATION: (1241). (3199)
OTHER INFORMATION: Cry3Bb1 variant 11231mv2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: terminator
LOCATION: (3217)...(3450)
OTHER INFORMATION: T-Ta.hspl7
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OTHER INFORMATION: P-CAMV.35S
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NAME/KEY: 5'UTR
LOCATION: (664)..(734)
OTHER INFORMATION: L-Ta.hcbl
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OTHER INFORMATION: I-OS.Act1
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Best Local Similarity
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NAME/KEY: promoter
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NAME/KEY: intron
LOCATION: (748)...
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US-11-192-801-23/c
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US-11-192-801-23
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TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 486; Conserv
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US-11-038-981A-22/c
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                           NAME/KEY: terminator
LOCATION: (3475)...(3730)
OTHER INFORMATION: Agrobacterium tumefaciens nos 3' transcription
OTHER INFORMATION: termination and polyadenylation sequence
                                                                                                                                              77;
                                                                                                                5.0%; Score 377.6; DB 7; Length 3754;
81.4%; Pred. No. 8.9e-56;
tive 0; Mismatches 34; Indels 77;
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Publication No. US20050283856A1

GENERAL INFORMATION:
APPLICANT: Conner, Timothy W.
APPLICANT: Fleathski, Stanislaw
APPLICANT: Pang, Sheng Z
APPLICANT: Pang, Sheng Z
TITLE OF INVENTION: GHIMBRIC PROMOTERS FOR USE IN PLANTS
FILE REFERENCE: 38-21(51446)B
CURRENT APPLICATION NUMBER: 05/11/038,981A
CURRENT FILING DATE: 2005-01-20
PRIOR FILING DATE: 2004-01-20
NUMBER OF SEQ ID NOS: 35
SEQ ID NO 21
LENGTH: 1467
OTHER INFORMATION: Cry3Bbl variant v11231
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                                                                                                                                               Matches 485; Conservative
                                                                                                                                  Similarity
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US-11-038-981A-21/c
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US-11-192-801-15
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                                                                                                                                  Gaps
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Publication No. US20050283856A1
GENERAL INPORMATION:
APPLICANT: Conner, Timothy W.
APPLICANT: Flasinski, Stanislaw
APPLICANT: Pang, Sheng Z
APPLICANT: Pong, Sheng Z
APPLICANT: Pang, Sheng Z
APPLICANT: NOW, Jinsong
FILE OF INVENTION: CHIMERIC PROMOTERS FOR USE IN PLA
CURRENT APPLICATION NUMBER: US/11/038,981A
CURRENT FILING DATE: 2005-01-20
PRIOR APPLICATION NUMBER: 60/537,793
PRIOR PILING DATE: 2004-01-20
NUMBER OF SEQ ID NOS: 35
                                                                                                                            38;
                                                                             DB 7;
                                                     5.0%; Score 376.2; DB 7
ilarity 80.9%; Pred. No. 1.2e-55;
Conservative 0; Mismatch.
), OTHER INFORMATION: Artificial promoter sequence US-11-038-981A-21
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Gaps

77;

Indels

34;

Mismatches

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Conservative
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LENGTH: 4149
481;
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                                                                               77;
                                                       Length 1467;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 6, Application US/11038981A
; Publication No. US20050283856A1
; Publication No. US20050283856A1
; GENERAL INFORMATION:
; APPLICANT: Conner, Timothy W.
; APPLICANT: Pang, Sheng Z
; APPLICANT: Pang, Sheng Z
; TITLE OF INVENTION: CHIMERIC PROMOTERS FOR USE IN PLANTS
; FILE REFERENCE: 38-21(51446)B
; CURRENT APPLICATION NUMBER: US/11/038,981A
; CURRENT FILING DATE: 2005-01-20
; PRIOR FILING DATE: 2004-01-20
                                                     Query Match 4.9%; Score 374.6; DB 7; Length Best Local Similarity 81.3%; Pred. No. 2.2e-55; Matches 482; Conservative 0; Mismatches 34; Indels
                                                                                                           6193 TATCACATCAATCCACTTGCTTTGAAGACGTGGAACGTCTTCT
 ; FEATURE:
; OTHER INFORMATION: Artificial promoter sequence
US-11-038-981A-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Cauliflower mosaic virus
                                                                                                                                                                                                                                                                                                                                                            GTTGAAAGTCTCA------
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SEQ ID NO 6
LENGTH: 524
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Best Local Similarity
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RESULT 9
US-11-192-801-13/c

i Sequence 13, Application US/11192801

sequence 13, Application US/11192801

publication No. US20050273882A1

GENERAL INFORMATION:

APPLICATUR: ROMANDO. Charles P.

TITLE OF INVENTION: Improved Exp. Corn

CURRENT APPLICATION NUMBER: US/11/192,801

CURRENT APPLICATION NUMBER: US/11/192,801

CURRENT FILING DATE: 2005-07-29

PRIOR FILING DATE: 1002-08-29

PRIOR FILING DATE: 1999-08-19

NUMBER OF SEQ ID NOS: 43

SOFTWARE: Patentin Ver. 2.0
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                                               524 ATCACATCAATCCACTTGCTTTGAAGACGTGGTTGGAACGTCTTCTTTTCCACGATGCT
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OTHER INFORMATION: P-CAMV.35S
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NAME/KEY: intron
LOCATION: (669)..(1472)
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GENERAL INFORMATION
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                                                                                                                                                                                                                                                                                          LOCATION: (3871)..(4127)
OTHER INFORMATION: T-AGRtu.nos 3' transcription termination and OTHER INFORMATION: polyadenylation sequence
                                                                                                                                                                                                                                                                                                                                                                  Length 4149;
                                                                                                                                                                                                                                                                                                                                                                                                33; Indels
                                                                                                                                                                                                                                                                                                                                                                 4.8%; Score 367.2; DB 7;
81.4%; Pred. No. 5.5e-54;
tive 0; Mismatches 33;
                                                                                                                                                     NAME/KEY: transit peptide
LOCATION: (1799)..(1885)
OTHER INFORMATION: carboxy terminus TS-Zm.rbcS
                                               LOCATION: (1489). (1535)
OTHER INFORMATION: amino terminal TS-Zm.rbcS
                                                                                                                                                                                                                NAME/KEY: CDS
LOCATION: (1885)..(3843)
OTHER INFORMATION: Cry3Bb1 variant v11231
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   OTHER INFORMATION: I-Zm.Hsp70
                                                                                                        LOCATION: (1636)..(1798)
OTHER INFORMATION: I-Zm.rbcS
                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 81.4
Matches 485; Conservative
               FEATURE:
NAME/KEY: trangit peptide
                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: terminator
                                                                                         NAME/KEY: intron
LOCATION: (1636).
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US-11-192-801-13
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Sequence 10, Application US/10391414 Publication No. US20050278799A1

RESULT 10 US-10-391-414-10/c

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APPLICANT: KATSURA, Koji
APPLICANT: KATSURA, Koji
HAPLICANT: KATSURA, Koji
TITLE OF INVENTION: Stress Induced Promoter Derived From Rice
TITLE OF INVENTION: Stress Induced Promoter Derived From Rice
CURRENT APPLICATION NUMBER: US/10/391,414
CURRENT APPLICATION NUMBER: US/202-377316
FRIOR APPLICATION NUMBER: JP 2002-377316
FRIOR FILING DATE: 2002-12-26
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.1
IENGTH: 835
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                                                                                                                                                                                                                                                                                                                                                                                                               Length 835;
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APPLICANT: Flasinski, Stanislaw
APPLICANT: Pang, Shenng Z
APPLICANT: Pang, Shenng Z
APPLICANT: Pang, Shenng Z
TITLE OF INVENTION: CHIMERIC PROMOTERS FOR USE IN PLANTS
TITLE OF INVENTION: CHIMERIC PROMOTERS FOR USE IN PLANTS
FILE REFERENCE: 38-21(51446)B
CURRENT FILING DATE: 2005-01-20
PRIOR APPLICATION NUMBER: 60/537,793
PRIOR PLILING DATE: 2004-01-20
NUMBER OF SEQ ID NOS: 35
SEQ ID NO 26
LENGTH: 1935
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4.0%; Score 303.6; DB 6;
Best Local Similarity 91.7%; Pred. No. 2.5e-43;
Matches 321; Conservative 0; Mismatches 29;
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; OTHER INFORMATION: Artificial promoter sequence
US-11-038-981A-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 26, Application US/11038981A; Publication No. US20050283856A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Cauliflower mosaic virus
US-10-391-414-10
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ORGANISM: Artificial Sequence
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Best Local Similarity
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NUMBER OF SEQ ID NOS: 35
SEQ ID NO 18
LENGTH: 1273
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                                     6468 ACTGTATCTTTGATATTCTTGGAGTAGACGAGAGTGTCGTGCTCCACCATGTTGGGGATC 6527
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                                                                       497 ACAGTAATATTTGTAAGCTTCGAAGGATAGTGGGATTGTGCGTCATCCCTTACGTCAGTG
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Publication No. US20050283856A1

GENERAL INPORMATION:
APPLICANT: Conner, Timothy W.
APPLICANT: Flaainski, Stanislaw
APPLICANT: Pang, Sheng Z
APPLICANT: You, Jinsong
TITLE OF INVENTION: CHIMERIC PROMOTERS FOR USE IN PLANTS
FILE REFERENCE: 38-21(51446)B
CURRENT PILLING DATE: 2005-01-20
PRIOR PILLING DATE: 2004-01-20
PRIOR PILLING DATE: 2004-01-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 18, Application US/11038981A

Publication No. US20050283856A1

GENERAL INFORMATION:
APPLICANT: Conner, Timothy W.
APPLICANT: Flasinski, Stanislaw
APPLICANT: Pang, Sheng Z
APPLICANT: Pang, Sheng Z

TITLE OF INVENTION: CHIMERIC PROMOTERS FOR USE IN PLANTS
FILE REFERENCE: 38-21(51446)B

CURRENT APPLICATION NUMBER: US/11/038,981A

CURRENT FILING DATE: 2005-01-20

PRIOR APPLICATION NUMBER: 60/537,793

PRIOR FILING DATE: 2004-01-20
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 40;
 Mismatches
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; ORGANISM: Cauliflower mosaic virus
US-11-038-981A-5
 ;
 Matches 142; Conservative
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SEQ ID NO 5
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US-11-038-981A-18/c
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APPLICANT: Flashiski, Stanislaw
APPLICANT: Flashiski, Stanislaw
APPLICANT: Pang, Sheng Z
APPLICANT: Pang, Sheng Z
APPLICANT: You, Jinsong Z
FILE REPRENCE: 38-21(51446)B
CURRENT APPLICATION UNMBER: US/11/038,981A
CURRENT FILING DATE: 2005-01-20
PRIOR APPLICATION NUMBER: 60/537,793
PRIOR PLING DATE: 2004-01-20
NUMBER OF SEQ ID NOS: 35
SEQ ID NO 20
                                                                                                                                                                                                                 Indels
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Pred. No. 3.1e-11;
                                                                           ; OTHER INFORMATION: Artificial promoter sequence US-11-038-981A-18
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; Sequence 19, Application US/11038981A
; Publication No. US20050283856A1
; GENERAL INFORMATION:
; APPLICANT: Conner, Timothy W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 20, Application US/11038981A; Publication No. US20050283856A1; GENERAL INFORMATION:
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 97.5%;
Matches 118; Conservative
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1.5%; Score 116.2; DB 7; Length 1281;
Best Local Similarity 97.5%; Pred. No. 3.2e-11;
Matches 118; Conservative 0; Mismatches 3; Indels 0;
APPLICANT: Flasinski, Stanislaw
APPLICANT: Pang, Sheng Z
APPLICANT: Pang, Sheng Z
APPLICANT: Pang, Sheng Z
FPLE CANT: You, Jinsong
TITLE OF INVENTION: CHIMERIC PROMOTERS FOR USE IN PLANTS
FILE REFERRNCE: 38-21(51446)B
CURRENT APPLICATION NUMBER: US/11/038,981A
CURRENT APPLICATION NUMBER: 00/537,793
PRIOR PILING DATE: 2004-01-20
NUMBER OF SEQ ID NOS: 35
DEQ ID NO 19
LENGTH: 1281
TYPE: DNA
ORGANISM: Artificial Sequence
FFATURE:
FFATURE:
OTHER INFORMATION: Artificial promoter sequence
US-11-038-981A-19
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9: /cgn2_6/ptodata/1/pubpna/USO3D_PUBCOMB.seq:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 89, Appli Sequence 5, Appli Sequence 6, Appli Sequence 95, Appli Sequence 95, Appli Sequence 95, Appli Sequence 109, Appli Sequence 109, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli Sequence 12, Appli Sequence 13, Appli Sequence 13, Appli Sequence 14, Appli Sequence 17, Appli Sequence 18, Appli Sequence 19, Appli Sequence 6, Appli	Sequence o, Applia Sequence 95, Appl Sequence 109, App Sequence 21, Appl
10 US-11-006-076-89 9 US-10-473-945-2 9 US-10-473-945-5 9 US-10-473-945-5 6 US-10-161-403-95 6 US-11-006-076-95 6 US-11-016-408-21 10 US-11-016-403-109 5 US-10-161-403-109 5 US-10-161-403-109 5 US-10-161-403-19 6 US-10-322-656-12 9 US-10-473-945-1 6 US-10-473-945-1 6 US-10-161-403-89 8 US-10-161-403-95 10 US-11-006-076-89	8 US-10-161-408-6 10 US-11-006-076-95 6 US-10-161-403-109 8 US-10-161-408-21
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ALIGNMENTS

RESULT 1 US-10-650-249-1 Sequence 1. Application US/10650249 Sequence 1. Application US/10650249 SEDICATION NO. US20040045055A1 GENERAL INFORMATION: APPLICANT: Neff, Michael M TITLE OF INVENTION: THE SIZE AND STATURE OF A PLANT TITLE OF INVENTION: THE SIZE AND STATURE OF A PLANT TITLE OF INVENTION: THE SIZE AND STATURE OF A PLANT FILE REFERENCE: WSHU 2064.1 CURRENT FILING DATE: 2003-08-28 PRIOR FILING DATE: 2002-08-02 NUMBER OF SEQ ID NOS: 20 SOFTWARE PATENTION OF SEQ ID NOS: 20 NUMBER OF SEQ ID NOS: 20 SOFTWARE PATENTION 3.1 LENGTH: 7580 TYPE: DNA CURRENT 7580 TYPE: DNA SOFTWARE SEQ ID NO 1 LENGTH: 7580 TYPE: DNA CURRENT ATABLOADS: A TABLOADS: A TABLOADS: A SOFTWARE SECO SEQ ID NO 1 LENGTH: 7580 TYPE: DNA CURRENT ASSOCIATION OF SECO SECO SECO SECO SECO SECO SECO SECO	Query Match 100.0%; Score 7580; DB 7; Length 7580; Best Local Similarity 100.0%; Pred. No. 0; Matches 7580; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy 1 AGCTCTATTAATTCAAGAGCAGCAAATAAAGCAAAAACTCAAAACCTAAAGCTAAATTTCTGA 60 	OY 61 ATATGAAAGGGGTTAGATAATCATTCTCTCAACTAGTTAAAAAAAGTAATGATAAAATTA 120 	OY 121 AAAACACAATGGATCAATTAAGAGACAGTAGTTTATGATATATAT	OY 181 GTTGACATCACAAAGATCAAAATAATGACCGGTAATTGCCCAAATACCAAGGCGACAATT 240	QY 241 CATGCGATATTCAAACACCTTAATGTCATTCAAATACTAAACTAACT	gy 301 CAAAGCTAGCTAGATTTTTCTCAAGTGAGCAACAGTCTAATTCTTCTGAAAAAACTTGTT 360
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Matches 1403; Conservative 0; Mismatches 1; Indels 0; Gaps 0; (4) TIGITTCGGATCAGATCACATCAATCCACTTGCTTTGAAGACGTGGTTGGAACGTCT 6236	4251 TAGTTTCGGATCTAGATATCACATCAACTTTTTTTTTTT	4191 ICTTITICCAGGAIGHICCTCGTGGTGGGGGG	4131 GCAICLIGAACGAIAGCCIIICCIIIAIGCGAAIGAGGCGAIGGAACGAAGGAGGAGGTT 641 6357 TTTTCTACTGTCCTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCGAGGAGGTTT 641 6071 TTTTCTACTTTTCTATTGAAGTGAAGATAGCTGGCAATGGAAGGAGGAGGTTT 401	6417 CCCGATATTACCCTTTGTAAAAGTCTCAATAGCCCTCTGGTCTTCTGACACTGTATCT 647	6477 TTGATATTCTTG	6537	6597	3771	6717 A 3711 A	y 6777 AAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTGATATTCTTGGAGTAGACG 6836	y 6837 AGAGTGTCGTGCTCCACCATGTTGGGGATCTAGATATCACATCAATCCACTTGCTTTGAA 6896 1591 AGAGTGTCGTGCTCCACCATGTTGGGGATCTAGATATCACATCAATCCACTTGCTTTGAA 3532	y 6897 GACGTGGAACGTCTTTTTCCACGATGTCCTCGTGGGTGGG	y 6957 ggaccactgroggragaggcatcttgaacgatagcctttcctttatcgcaatgatggcat 7016	y 7017 ITGIAGAAGCCATCTTCCTTTCTACTGTCCTTTCGATGAGTGACAGATAGCTGGGCAA 7076	y 7077 IGGAATCCGAGGGTTTCCCGATATTACCCTTTGTTGAAAGTCTCAATAGCCCTCTGG 7136.	y 7137 ICTICIGAGACIGIAICTITGATAITCTIGAGAGAGAGAGAGIGICGIGCTCCACCAIG 7196	y 7197 TIGGGGAICTIAGATAICACAICAATCCACTIGCTITIGAACGIGGTIGGAACGICTICI 7256
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5513 GTAATGTATATTAAACGTACTTAAGTCGAATTTTATGACCAAAGTAAATTATGCCG 557	DD 1141 AAIGIAGAAGGAACIACAAAITTAAACAAAAAAAAAAAAA	5633	Qy 5693 TITCCCAAGACACAAAAAAAAAAAATACAGAAACGAAAAAAAGAGATTTTAAAAATTCA 5752 	Qy 5753 TAACCCACGAGAATTATGCACCTAAATTCAGACTAATCCCCCAAATTCAGAAATTTATG 5812 	Oy 5813 TATTTTGCGATTTAATATTGTGTTCACAATCATAATGGCCAACTAACT	Qy 5873 CAATGGAATGAAACCATGCATAATCTCTCAAGTCTCAACCTATGAAGAATCATGTA 5932 	OY 5933 ACCAATAGACTATCATCATGATTAATGCATGATCTATAATGTATTCTTTGAACATA 5992	Qy 5993 GATATGICALTIACTGGALATAAAGATGGCGTTTTAACCTACTTTGCAATTTTTGTTAT 6052	611	Qy 6113 TTTCAAACATCGATCACATTTTTACTTTTCCATATTGACTACATTTATAGGCTCAC 6172 bb 1681 TTTCAAACATCGATCACATTTTTACTTTTGTTTCCATATTGACTACATTTATAGGCTCAC 1740	Qy 6173 ACTTTT 6178 Db 1741 ACTTTT 1746	RESULT 3 US-10-033-190-3/c ; Sequence 3, Application US/10033190	; Publication No. US20020133848A1 ; GENERAL INFORMATION: ; APPLICANT: Exelixis Plant Sciences, Inc. ; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF AN ANTHOCYANIN MUTANT (ANT	; TITLE OF INVENTION: TOMATO ; FILE REPERENCE: EPO1-002C ; CURRENT APPLICATION NUMBER: US/10/033,190 ; CURRENT FILING DATE: 2001-10-29	; PRIOR APPLICATION NUMBER: US 60/244,685 ; PRIOR FILING DATE: 2000-10-30 ; SOFTWARE: PatentIn version 3.1	; SEQ ID NO 3 ; LENGTH: 10078 ; TYPE: DNA ; ORGANISM: pAG3202	US-10-033-190-3 Query Match Best Local Similarity 99.9%; Pred. No. 4.9e-245;

	6479 GATATTCTTGGAGTAGACAGAGTGTCGTGCTCCACCATGTTGGGGATCTAGATATCACA 6538	6539 TCAATCCACTTGCTTTGAAGACGTGGTTGGAACGTCTTCTTTTTCCACGATGTTCCTCGT 6598	GGGTGGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCATCTTGAACGATAGCCTTTCC	940 GGGTGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCATCTTGAACGATAGCCTTTCC 881 6659 TTTATCGCAATGATGGATTTGTAGAGGCCATCTTCCTTTTCTACTGTCCTTTCGATGAA 6718	880 TITARICGCAATGATGGCATTIGTAGAAGCCATCTTTCTTTCTACTGTCCTTTCGATGAA 821 6719 GTGACAGAATAGCCAATGGAATCGAAGGAGGTTTCCCGATATTACCCTTTTGTTGAAA 6778	GTGACAGATAGCTGGGCAATGGAATCCGAGGGGTTTCCCGATATTACCCTTTGTTGAAA	6779 AGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTGATATTCTTGGAGTAGACGAG 6838	AGTGTCGTCCTCCACCATGTTGGGGATCTAGATATCACATCAATCCACTTGCTTTGAAGA	6899 CGTGGTTGGAACGTCTTCTTTTCCACGATGTTCCTCGTGGGTGG			7079 GAATCCGAGGAGGTTTCCCGATATTACCCTTTGAAAAGTCTCAATAGCCCTCTGGTC 7138 	7139 TICTGAGACTGTATCTTGATATTCTTGGAGTAGACGAGAGTGTCGTGCTCCACCATGTT 7198		7259 TTCCACGAIGTTCCTCGTGGGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCATC 7318	7319 ITGAACGATAGCCTTTATCGCAATGATGACGCATTGTAGAAGCCATCTTCCTTTTC 7378 	7379 TACTGTCCTTTCGATGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCCCGA 7438 	7439 TATTACCCTTTGTTGAAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTGAT 7498	
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7257 TITICCACGATGTTCCTCGTGGGTGGGGTCCATCTTTGGGACCACTGTCGGTAGAGCA 731	Db 3171 TTTTCCACGATGTTCCTCGTGGGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCA 3112 Qy 7317 TCTTGAACGATAGCCTTTCCTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCCTTT 7376	Db 3111 TCTTGAACGATAGCCTTTCCTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCCTTT 3052	3051 TCTACTGTCCTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCCC 299	OY 7437 GATATTACCTTTGTTGAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTG 7496 Db 2991 GATATTACCTTTGTTGAAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTG 2932	Oy 7497 ATATTCTTGGAGTAGACGAGAGTGTCGTCCACCACCATGTGGGGATCCACTAGTTCTAG 7556 NA 2031 ANAMIC CONTRACTAGA CASAGAG CONTRACTAGA CONTRACTAGA CASAGA CASAGA CONTRACTAGA CANAGA CASAGA CASAGA CONTRACTAGA CASAGA	7557 AGGGGCGCGCGGGGGGGGT 7580	Db 2871 AGCGGCCGCCACCGCGGTGGAGCT 2848	RESULT 4 US-09-522-334-1/c ; Sequence 1, Application US/09522334 ; Patent No. US20020157130A1	; GENERAL INFORMATION: ; APPLICANT: Wagner, Ry ; APPLICANT: Mathews, Helena . applicant: i.i. ying liang	APPLICANT: Waggoner, Wency J. TITLE OF INVENTION: TEATT-ASSOCIATED GENE IDENTIFICATION TITLE OF INVENTION: METHOD FILE REFERENCE: 4257-0018.30	CURRENT APPLICATION NUMBER: US/09/522,334 CURRENT FILING DATE: 2000-03-09 PRIOR APPLICATION UNMBER: US 60/124,232 PRIOR FILING DATE: 1999-03-12	; NUMBER OF SEQ ID NOS: 28 ; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 1 ; LENGTH: 1361	; TYPE: DNA CRGANISM: Artificial Sequence ; FRATURE: ; OTHER INFORMATION: modified enhancer	OS-09-522-534-1 Query Match 17.9%; Score 1360; DB 3; Length 1361; Best Local Similarity 100.0%; Pred. No. 1.1e-237. Marchea 1360: Concervative O. Mismatchea O. Indels O. Gans O:	6179 GTTTCGGATCTAGATATCACATCACTTGCTTTGAAGACGTGGTTGGAACGTCTTTC	Db 1360 GTTTCGGGATCTAGATATCACATCACTCACTTGCTTTGAAGACGTGGTTGGAACGTCTTC 1301 Qy 6239 TTTTCCACGATGTTCCTCGTGGGTGGGGTCCATCTTTGGGACCACTGTGGTAGAGGC 6298 Db 1200 FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	6299 ATCTTGAAGGATAGCCTTTCCTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCCTTTCTTCTTTCT	6359 TTCTACTGTTTCGATGAAGTGACAGATAGCTGGCAATGGAATCCGAGGAGGTTTCC 1180 TTCTACTGTTTCGATGAAGTGACAGATAGCTGGCAATGGAATCCGAGGAGGTTTCC 1180 TTCTACTGTCCTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCC	OY 6419 CGATATTACCCTTTGTTGAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTT 6478

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RESULT 6
US-10-650-249-20

Sequence 20, Application US/10650249

Sequence 20, Application No. US20040045055A1

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: THE SIZE AND STATURE OF A PLANT

TITLE OF INVENTION: THE SIZE AND STATURE OF A PLANT

FILE REPERENCE: WSHU 2664.1

CURRENT APPLICATION NUMBER: US/10/650,249

PRIOR PEPLICATION NUMBER: US 60/406,657

PRIOR FILING DATE: 2002-08-02

NUMBER OF SEQ ID NOS: 20

SOFTWARE: Patentin version 3.1
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                                                                                                   CTTGTCATGCGAGTTATTGCTGAGGAAGATCAAACCATGCAGCTATATCCAAAGGCTAAT 5236
TTTTGTCTCCGACCAATGTTTCAAACTCGAATCCTTTCGTTAAAAGTTGTTTCTGCTTTA
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100.0%; Pred. No. 2.1e-183;
tive 0; Mismatches 0;
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                                                                 Sequence 17, Application US/10650249
Publication No. US20040045055A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Neff, Michael M
TITLE OF INVENTION: THE GENE FOR A DOF TRANSCRIPTION FACTOR CAPABLE OF ALTERING
TITLE OF INVENTION: THE SIZE AND STATURE OF A PLANT
FILE REFERENCE: WSHU 2064.1
CURRENT APPLICATION NUMBER: US/10/650,249
CURRENT FILING DATE: 2003-08-28
PRIOR FILING DATE: 2003-08-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
SEQ ID NO 17
LENGTH: 1235
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US-10-650-249-17
                                               RESULT 5
US-10-650-249-17
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Sequence 19, Application US/10650249
Publication No. US20040045055A1
GENERAL INFORMATION:
APPLICANT: Neff, Michael M
TITLE OF INVENTION: THE GENE FOR A DOF TRANSCRIPTION FACTOR CAPABLE OF ALTERING
TITLE OF INVENTION: THE SIZE AND STATURE OF A PLANT

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100.0%; Pred. No. 1.2e-182;
ative 0; Mismatches 0;
FILE REFERENCE: WSHU 2064.1
CURRENT APPLICATION NUMBER: US/10/650,249;
CURRENT FILING DATE: 2003-08-28;
FRIOR APPLICATION NUMBER: US 60/406,657;
FRIOR FILING DATE: 2002-08-02;
NUMBER OF SEQ ID NOS: 20;
SOFTWARE: PatentIn version 3.1
SERGIP NO 19
LENGTH: 1058
                                                                                                                            ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-650-249-19
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APPLICANT: Mendel Biotechnology, Inc.
APPLICANT: MANCHER, Oliver
APPLICANT: RECHMANN, Jose Luis
APPLICANT: RECHMANN, Jose Luis
APPLICANT: RECHMANN, Jose Luis
APPLICANT: DUBELL, Arnold T
APPLICANT: DUBELL, Arnold T
APPLICANT: HEARD, Jacqueline E
APPLICANT: HEARD, Jacqueline E
APPLICANT: HEARD, Cai-Zhong
APPLICANT: GIAGR, Cai-Zhong
APPLICANT: BIGBR, Cai-Zhong
APPLICANT: PIKEDA, Omaira
APPLICANT: PIKEDA, Omaira
APPLICANT: PIKEDA, Omaira
APPLICANT: WOU Liang
APPLICANT: WOU Liang
APPLICANT: WOU Liang
APPLICANT: BROWN, Pierre E
APPLICATION WIMBER: 09/837,444
BRIOR FILING DATE: 2001-08-09
PRIOR FILING DATE: 2001-08-09
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Pred. No. 5.7e-116;
0; Mismatches 0; Indels S
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Best Local Similarity 89.5%;
Matches 795; Conservative
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APPLICANT: Neff, Michael M
TITLE OF INVENTION: THE GENE FOR A DOF TRANSCRIPTION FACTOR CAPABLE OF ALTERING
TITLE OP INVENTION: THE SIZE AND STATURE OF A PLANT
FILE REFERENCE: WSHU 2064.1
CURRENT APPLICATION NUMBER: US/10/650,249
FILE REFERENCE APPLICATION NUMBER: US 60/406,657
PRIOR FILING DATE: 2002-08-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATENTIN version 3.1
SEQ ID NO 12
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                           841 GITIAAAGITACTATGACTITAAICTGAGITATTITATCCATTITCTITTIGCAGCTTIGT
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                                                                                                                                                                                                                                                                                             1021 TTATAAACCTGAAACTAATTAGTACAAATTATGTTAAT 1058
                                                                                                                                                                                                                                                                    4065 TTATAAACCTGAAACTAATTAGTACAAATTATGTTAAT 4102
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12, Application US/10650249; Publication No. US20040045055A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-650-249-12
                                                                                                                                                                                                                                                                                                                                                                                            RESULT 8
US-10-650-249-12
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APPLICANT: Ratcliffe, Oliver
APPLICANT: Radam, Luc J
APPLICANT: Redde, James
APPLICANT: Redde, James
APPLICANT: Redde, James
APPLICANT: Redde, James
APPLICANT: Broun, Pierre E
APPLICANT: Pilgrim, Marcha L
CURENT FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 09/934, 455
PRIOR APPLICATION NUMBER: 60/336,049
PRIOR FILING DATE: 2001-10-19
PRIOR FILING DATE: 2001-11-19
PRIOR FILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: 60/336,049
PRIOR FILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: 10/11,468
PRIOR FILING DATE: 2001-12-11
PRIOR FILING DATE: 2002-06-14
PRIOR FILING DATE: 2002-06-09
PRIOR FILING DATE: 2002-06-09
PRIOR FILING DATE: 2002-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Arabidopsis thaliana
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US-10-374-780A-2767
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                                                                                                                                        4292 AGAIGIGACTCAACCAAITCTAGTTACTTCAATAACTATAGCCTTACTCAACCT
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                                                                      4232 ATGGTGGAACGTGCTCGGATCGCAAAAGTCCCATTGCCTGAAGCAGCTCTAAATTGCCCT
                                     Gaps
                                    93;
Length 795;
                                    Indels
 Query Match 9.1%; Score 692; DB 7; L
Best Local Similarity 89.5%; Pred. No. 5.7e-116;
Matches 795; Conservative 0; Mismatches 0;
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Sequence 2767, Application US/10374780A
Publication No. US20040019927A1
GENERAL INFORMATION:
APPLICANT: Sherman, Bradley K
APPLICANT: Riechmann, Jose Luis
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Heard, Jacqueline E
APPLICANT: Heard, Jacqueline E
APPLICANT: Heard, Volker
APPLICANT: Creelman, Robert A

RESULT 10 US-10-374-780A-2767

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Sequence 15, Application US/10650249
Publication No. US20040045055A1
GENERAL INFORMATION:
APPLICANT: Neff, Michael M
TITLE OF INVENTION: THE GENE FOR A DOF TRANSCRIPTION FACTOR CAPABLE OF ALTERING; TITLE OF INVENTION: THE SIZE AND STATURE OF A PLANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGGIGCAAICTICAAACGCGIIAIAICCAIIACIAGAAGGIAAGGGAGGIGTIAAICAA 4831
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                                                                                         4232 ATGGTGGAACGTGCTCGGATCGCAAAAGTCCCCATTGCCTGAAGGAGCTCTAAATTGCCCT
                                                                                                                4292 AGATGTGACTCAACCAATACTAAGTTCTGTTACTTCAATAACTATAGCCTTACTCAACCT
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                    Pred. No. 5.7e-116;
0; Mismatches 0;
  DB 9;
    Score 692;
  9.1%;
                         Best Local Similarity 89.5
Matches 795; Conservative
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APPLICANT: ADAM, Luc J
APPLICANT: ADAM, Luc J
APPLICANT: ADAM, Luc J
APPLICANT: DUBELL, Arnold T
APPLICANT: DUBELL, Arnold T
APPLICANT: DUBELL, Arnold T
APPLICANT: PILGRIM, Marsha L
APPLICANT: PILGRIM, Marsha L
APPLICANT: PILGRIM, Marsha L
APPLICANT: PILGRIM, Marsha L
APPLICANT: PILGRIM, Robert A
APPLICANT: PINEDA, Omaira
APPLICANT: BOOWN, Pierre E
TITLE OF INVENTION: Yield-Related Polynucleotides and Polypeptides in Plants
FILE REFERENCE: MBIO036-2 US
FILE REFERENCE: MBIO036-2 US
FRICK APPLICATION NUMBER: 09/837, 444
FRICK FILING DATE: 2001-04-18
FRICK APPLICATION NUMBER: 60/316, 049
FRICK PILING DATE: 2001-12-05
FRICK APPLICATION NUMBER: 60/336, 049
FRICK FILING DATE: 2001-12-11
FRICK APPLICATION NUMBER: 60/336, 049
FRICK PILING DATE: 2001-12-11
FRICK PILING DATE: 2002-06-14
SHOR PILING DATE: 2002-06-14
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                                421 GGAACTCAAATAAGCAACATGATAAGTGGTATGTTCTAGTGGGGATCTTGGATGCA
                                                                                             TGGAGAATACCTCCATCACAACAAGCTCAGCAATTCCCTTTCTTGATCAACACTACCGGA
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Publication No. US20050160493A9
GENERAL INFORMATION:
APPLICANT: Mendel Biotechnology, Inc.
APPLICANT: RATCLIFFE, Oliver
APPLICANT: RIECHMANN, Jose Luis
APPLICANT: ADAM, Luc J
APPLICANT: DIBELL, Arnold T
APPLICANT: PICRIM, Marsha L
APPLICANT: PICRIM, Marsha L
APPLICANT: JIANG, Cai-Zhong
APPLICANT: JIANG, Cai-Zhong
APPLICANT: REUBER, T. Lynne
APPLICANT: REUBER, T. Lynne
APPLICANT: PINEDA, Omalira
APPLICANT: PINEDA, Omalira
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; ORGANISM: Arabidopsis thaliana
US-10-225-066A-409
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US-10-225-066A-409
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                                                                                                                                                                        Length 684;
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                                                                                                                                                                    Query Match 9.0%; Score 684; DB 7; Le
Best Local Similarity 100.0%; Pred. No. 1.5e-114;
Matches 684; Conservative 0; Mismatches 0;
FILE REFERENCE: WSHU 2064.1

CURRENT APPLICATION NUMBER: US/10/650,249

CURRENT FILING DATE: 2003-08-28

FRIOR APPLICATION NUMBER: US 60/406,657

PRIOR PILING DATE: 2002-08-02

NUMBER OF SEQ ID NOS: 20

SOFTWARE: PatentIn version 3.1

SOFTWARE: 684
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                                                                                                                   ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-650-249-15
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Sequence 90, Application US/10161403; Publication No. US20030119104A1; GENERAL INFORMATION: APPLICANT: Perkins, Edward; APPLICANT: Perez, Carl

RESULT 13 US-10-161-403-90

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Pred. No. 7.3e-102;
0; Mismatches 33;
APPLICANT: Lindenbaum, Michael
APPLICANT: Greene, Amy
APPLICANT: Leung, Josephine
APPLICANT: Leung, Josephine
APPLICANT: Leung, Josephine
APPLICANT: Stewart, Sandra
APPLICANT: Shellard, Joan
TILLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
FILE REPRERENCE: 24601-420
CURRENT FILING DATE: 2002-05-30
CURRENT FILING DATE: 2002-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2002-03-21
NUMBER OF SEQ ID NOS: 129
SOFTWARE: RestSEQ for Windows Version 4.0
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Best Local Similarity 93.6%;
Matches 659; Conservative (
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                                                                                                  7528 CCACCATGTTGGGGATCCACTAGTTCTAGAGCGGCCGCCACCGC 7571
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Pred. No. 7.3e-102;
0; Mismatches 33;
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APPLICANT: Perez, Carl
APPLICANT: Lindenbaum, Michael
APPLICANT: Lindenbaum, Michael
APPLICANT: Lindenbaum, Michael
APPLICANT: Fleming, Blena
APPLICANT: Fleming, Blena
APPLICANT: Fleming, Blena
APPLICANT: Stewart, Sandra
APPLICANT: Shellard, Joan
TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
FILE BEFERRACE: 17084-022002/4208
CURRENT APPLICATION NUMBER: US/11/006,076
CURRENT APPLICATION NUMBER: 60/294,758
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2002-03-21
NUMBER OF SEQ ID NOS: 129
SEQ ID NO 90
LENGTH: 8428
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; OTHER INFORMATION: pCambia3300 Plasmid
US-11-006-076-90
                                                                                                                                                                                                            ; Sequence 90, Application US/11006076; Publication No. US20050181506A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 93.6%;
Matches 659; Conservative
                                                                                                                                                                                 RESULT 15
US-11-006-076-90
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      7794 CCACCATGTTGGCAAGCTGCTCTAGCCAATACGCAAAACCGCCTC 7837
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                                                                                             US-LU-101-400-4

Sequence 2, Application US/10161408

Publication No. US20040214290A1

GENERAL INFORMATION:

APPLICANT: Fabijanski, Steven

APPLICANT: Fabijanski, Steven

APPLICANT: Perkins, Edward

TITLE OF INVENTION: Plant Artificial Chromosomes,

TITLE OF INVENTION: Plant Artificial Chromosomes

FILE REFERENCE: 24601-419

CURRENT APPLICATION UNMERR: US/10/161,408

CURRENT FILING DATE: 2001-05-30

PRIOR APPLICATION NUMBER: US 60/294,687

PRIOR APPLICATION NUMBER: US 60/296,329

PRIOR FILING DATE: 2001-06-04

NUMBER OF SEQ ID NOS: 51

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 2

LENGTH: 8428
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93.6%; Pred. No. 7.3e-102;
tive 0; Mismatches 33;
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                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 93.6
Matches 659; Conservative
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US-10-161-408-2
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Search completed: December 31, 2005, 06:23:45 Job time : 3577 secs

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1603 HANDAN ISH

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MOLECULE TYPE: synthetic DNA DESCRIPTION: transformation plasmid pPHI1406
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/cgn2_6/ptodata/1/ina/6_COMB.seq:*
/cgn2_6/ptodata/1/ina/6_COMB.seq:*
/cgn2_6/ptodata/1/ina/H_COMB.seq:*
/cgn2_6/ptodata/1/ina/H_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/RE_COMB.seq:*
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Compugen Ltd.
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US-09-011-151-9

US-09-011-151-9

US-09-623-551-17

US-09-810-861B-4

US-09-737-69BB-29

US-09-737-69BB-29

US-09-737-69B-29

US-10-427-169-29

US-10-427-169-29

US-09-737-69B-30

US-09-737-69B-30

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US-09-441-340-25
US-09-441-340-31
US-09-377-466B-23
US-10-232-665-23
US-09-377-466B-15
                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                          1303057 seqs, 888780828 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
GenCore version
Copyright (c) 1993 - 2005
                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                nucleic search, using sw model
                                                                                                                                                                       IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length DB
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TITLE OF INVENTION: MAIZE CHLOROTIC DWARF VIRUS RESISTANCE
NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:
ADDRESSEE: Pioneer Hi-Bred International, Inc.
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CITY: Dea Moines
STATE: 10wa
COUNTRY: United States
ZIP: 50.30
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS, Microsoft Windows
SOFTWARE: Microsoft Windows No. 5569828epad
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/038,768A
FILING DATE: 19930324
CLASSIFICATION NUMBER: 29,344
FILING DATE: 29,342
REGISTRATION NUMBER: 0235 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (515) 245-3594
TELEFAX: (515) 245-3634
INFORMATION FOR SEG ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGER: MARCHERISTICS:
MARCHERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Pioneer Hi-Bred International, Inc
STREET: 700 Capital Square, 400 Locust
US-10-232-665-15

US-09-182-117-1

US-09-186-002-16

US-09-186-002-16

US-09-434-039A-5

US-09-434-039A-5

US-09-182-117-4

US-09-186-002-14

US-09-186-002-13

US-09-186-002-13

US-09-186-002-13

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US-09-097-319A-19

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                                            Conservative
                                Similarity
                     Query Match
Best Local Simi
Matches 659;
 US-09-577-424-1
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APPLICANT: Rhoads, David M
TITLE OF INVENTION: METHOD FOR IDENTIFYING COMPONENTS INVOLVED IN SIGNAL
TITLE OF INVENTION: TRANSDUCTION PATHWAYS IN HIGHER PLANTS
FILE REFERENCE: UNL2990
CURRENT PAPLICATION NUMBER: US/09/577,424
CURRENT FILING DATE: 2000-05-22
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 1
LENGTH: 12614
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                                                         1043 TGCTCCTCGTGGGTGGGGGTCCATCTTTGGGACCACTGTCGCAGAGGCATCTTGAACGA
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                                           6868 AGATATCACATCAATCCACTTGCAAGACGTGGTTGGAACGTCTTTTTTCCACGA
                                                                                       6928 TGTTCCTCGTGGGTGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCATCTTGAACGA
                                                                                                                                   TAGCCTTTCCTTTATCGCAATGATGCCATTTGTAGAAGCCATCTTCCTATTTCTACTGTCC
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                        Gaps
                        4;
Length 5033;
 Score 621; DB 2; Length 50 Pred. No. 2.8e-111; 0; Mismatches 30; Indels
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Patent No. 6525245
 8.2%;
            al Similarity 95.1
653; Conservative
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NAME/KEY: CDS
LOCATION: (1665)..(3317)
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US-09-577-424-1/c
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                                             12;
    Length 12614;
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                                             Indels
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US-08-836-402B-7/c
; Sequence 7, Application US/08836402B
; Patent No. 6643988
; GENERAL INFORMATION:
APPLICANT: Rudiger Hain, Regina Fischer
TITLE OF INVENTION:
CORRESPONDENCE ADDRESS:
ADDRESSEE: SPRUNG KRAMER SCHAFFER & BRISCOE
STREET: 660 White Plains Road
CITY: Tarrytown
STATE: New York
COUNTRY: U.S.A.
ZIP: 10591-5144
COMPUTER: RADABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB storage
COMPUTER: Gateway 2000
Score 617.2; DB 3;
Pred. No. 1.9e-110;
0; Mismatches 33;
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6308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.3%; Score 554.2; DB 3; Length 1138; 92.3%; Pred. No. 1.9e-98; Indels 14; ive 0; Mismatches 38; Indels 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6190 AGATATCACATCAATCCACTTGCTTTGAAGACGTGGTTGGAACGTCTTC-
                                                    RESULT 4
US-09-011-151-8/C

Sequence 8, Application US/09011151
Fatent No. 6380463
GENERAL INFORMATION:
APPLICANT: Jepson, Ian
TITLE OF INVENTION: DNA CONSTRUCTS
FILE REFERENCE: PPD 50059/UST
CURRENT PILING DATE: 1998-01-29
FRIOR APPLICATION NUMBER: PCT/GB96/01883
PRIOR APPLICATION NUMBER: CT/GB96/01883
PRIOR APPLICATION NUMBER: GB 9515941.4
PRIOR PILING DATE: 1996-08-03
PRIOR FILING DATE: 1996-08-03
PRIOR PILING DATE: 1995-08-03
WUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn version 3.0
  39 AGCCCTCTGGTCTTCTGAGAC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
; OTHER INFORMATION: Plasmid pMJB1
US-09-011-151-8
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Matches 621; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial
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97.7%; Pred. No. 4.6e-100;
                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,402B
FILING DATE: 02-SEP-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION UNMER: 44 40 200.7 (Germany)
FILING DATE: 10-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Kurf G. Briscoe
REGISTRATION NUMBER: 33,141
REFERENCE/DOCKET NUMBER: Bayer 9840-KGB
TELEPONE: (914) 332-1700
TELEPHONE: (914) 332-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6788 AGCCCTCTGGTCTTCTGAGAC 6808
SYSTEM: DOS
Microsoft Windows 98
                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 2728 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 97.73
Matches 607; Conservative
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Sequence 17, Application US/09623551

Sequence 17, Application US/09623551

Patent No. 6774281

GENERAL INFORMATION:

APPLICANT: Stuiver, Maarten

APPLICANT: Stuiver, Jerome

APPLICANT: Stuiver, Jerome

TITLE OF INVENTION: Method For The Induction Of Pathogen Resistance In

TITLE OF INVENTION: Plants

TITLE OF INVENTION: Plants

TITLE OF INVENTION: Plants

FILE REFERENCE: MOG57706/UST

CURRENT APPLICATION NUMBER: US/09/623,551

CURRENT PILING DATE: 1998-03-06

PRIOR FILING DATE: 1999-03-08

PRIOR FILING DATE: 1999-03-08

NUMBER OF SEQ ID NOS: 29

SEQ ID NO 17

FERMINE PATENTION NOWER: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5310 TAGCCTTTCCTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCCTTTTCTACTGTCC 6369
986 AGCTGGGCAATGGAATCCGAGGAGGTTTCCGGATATTACCCTTTGTTGAAAAGTCTCAAT 1045
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                                     6788 AGCCCTCTGGTCTTCTGAGACTGTATCTTGATATTCTTGGAGTAGACGAGAGTGTCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence:Combination; OTHER INFORMATION: 35S Promoter with the Glucanase II leader US-09-623-551-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 104;
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Pred. No. 1.4e-80;
0; Mismatches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
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ilarity 80.4%;
Conservative (
                                                                                                           6848 CICCACCATGITG 6860
                                                                                                                                    1106 CTCCACCATGTTG 1118
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US-09-623-551-17/c
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        93 TGCCCTTTGGTCTTCTGAGACTGTATCTTTGATATTTTTGGAGTAGACAAGTGTGTCGTG 34
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                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Jepson, lan
TITLE OF INVENTION:
FILE REFERENCE: PPD 50059/UST
CURRENT APPLICATION NUMBER: US/09/011,151
CURRENT FILING DATE: 1998-01-29
PRIOR APPLICATION NUMBER: PCT/GB96/01883
PRIOR APPLICATION NUMBER: GB 9515941.4
PRIOR PLING DATE: 1995-08-03
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN OF SEQ ID NOS: 33
SOFTWARE: PATENTIN VERSION 3.0
                                                                                                                                                              Sequence 9, Application US/09011151
Patent No. 6380463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTHER INFORMATION: Plasmid pMJB1
US-09-011-151-9
                                              6860
                                                                              21
                                                                                CTCCACCATGTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1138
                                                                                                                                  RESULT 5
US-09-011-151-9
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Best Local Similarity
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APPLICANT: Morey, Teafrir S.

APPLICANT: Soreq, Hermona

APPLICANT: Arntzen, Charles J.

APPLICANT: Mason, Hugh S.

TITLE OF INVENTION: EXPRESSION OF RECOMBINANT HUMAN ACETYLCHOLINESTERASE IN

TITLE OF INVENTION: TRANSGENIC PLANTS

FILE REFERENCE: BIT-45

CURRENT APPLICATION NUMBER: US/09/810,861B

CURRENT APPLICATION NUMBER: 60/190,440

PRIOR APPLICATION NUMBER: 60/190,440

PRIOR APPLICATION NUMBER: 60/190,440

PRIOR ELLING DATE: 2000-03-17

NUMBER OF SEQ ID NOS: 5

SEQ ID NO 3

LENGTH: 5767
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346 TITGAATCTTTGACTCCATGCGGAATTATCACATCAATCCACTTGCTTTGAAGACGTGGT 287
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                                                                                                                           226 GTCGGCAGAGGCATCTTCAACGATGGCCTTTTCTTTATCGCAATGATGGCATTTGTAGGA
                                                      166 GCCACCTTCCTTTTCCACTATCTTCACAATAAAGTGACAGATAGCTGGGCAATGGAATCC
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US-09-810-861B-3
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Best Local Similarity 86.5%; Pred. No. 3.9e-80;
Matches 582; Conservative 0; Mismatches 0.
                                                                                                                                                                                                                                                                                                                  GACTGTATCTTGATATTCTTGGAGTAGA 6834
                                                                                                                                                                                                                                                                                                                                                   46 GACTGTATCTTTGATATTTTTGGAGTAGA 18
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; Sequence 3, Application US/09810861B
; Patent No. 6770799
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ORGANISM: Artificial Sequence
FEATURE:
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US-09-810-861B-4/C

US-09-810-861B-4/C

Sequence 4, Application US/09810861B

Patent No. 6770799

GENERAL INFORMATION:

APPLICANT: Mory Tasfrir S.

APPLICANT: Mory Hermona

APPLICANT: Arntzen, Charles J.

APPLICANT: Macon, Hugh S.

TITLE OF INVENTION: EXPRESSION OF RECOMBINANT HUMAN ACETYLCHOLINESTERASE IN

TITLE OF INVENTION: EXPRESSION OF RECOMBINANT HUMAN ACETYLCHOLINESTERASE IN

TITLE OF INVENTION: EXPRESSION OF RECOMBINANT HUMAN ACETYLCHOLINESTERASE IN

TITLE OF INVENTION: EXPRESSION OF RECOMBINANT HUMAN ACETYLCHOLINESTERASE IN

TITLE OF INVENTION: EXPRESSION OF RECOMBINANT HUMAN ACETYLCHOLINESTERASE IN

TITLE OF INVENTION: EXPRESSION OF RECOMBINANT HUMAN ACETYLCHOLINESTERASE IN

TITLE OF INVENTION: EXPRESSION OF RECOMBINANT HUMAN ACETYLCHOLINESTERASE IN

TITLE OF INVENTION: DATE: 2001-03-16

PRIOR PRICATION NUMBER: 60/190,440

PRIOR APPLICATION NUMBER: 60/190,440

PRIOR APPLICATION NUMBER: 60/190,440

PRIOR APPLICATION OF SEQ ID NOS: 5

SOFTWARE: PATENTION OF SEQ ID NOS: 5 PEATURE:
NAME/KRY: misc feature
LOCATION: (11862)..(12157)
OTHER INFORMATION: Description of Artificial Sequence: plasmid vector
OTHER INFORMATION: pTM036. Identity of sequence residues 11862-12157 unknown. 6249 6308 33 92 AGCCCTCTGGTCTTCTGAGACTGTATCTTTGATATTCTTGGAGTAGACGAGAGTGTCGTG CCATCTTTGGGACCACTGTCGGTAGAGGCATTCTTGAACGATAGCTTTCCTTTATCGCA 6668 ATGATGGCATTTGTAGAAGCCATCTTCCTTTTCTACTGTCCTTTTCGATGAAGTGACAGAT 212 ATGATGGCATTTGTAGAAGCCATCTTCCTTTCTACTGTCCTTTCGATGAAGTGACAGAT 152 AGCTGGGCAATGGAATCCGAGGAGGTTTCCCGATATTACCCTTTGTTGAAAAGTCTCAAT 6190 AGAIATCACATCAATCCACTTGCTTTGAAGACGTGGTTGGAACGTCTTCTTTTTCCACGA TGTTCCTCGTGGGGGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCA-TCTTGAACG Gaps

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LOCATION: (1)..(1800)
OTHER INFORMATION: y = t/u or c
OTHER INFORMATION: chimeric promoter fusion CaMV and Act8 polynucleotides +
OTHER INFORMATION: tro
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| Batent No. 6660911
| GENERAL INFORMATION:
| APPLICANT: Fincher, Karen
| APPLICANT: Fincher, Stanislaw
| APPLICANT: Fincher, Stanislaw
| APPLICANT: Wilkinson, Jack
| TITLE OF INVENTION: No. 6660911e1 Plant Expression Constructs
| FILE REFERENCE: 38-21(51499)
| FILE REFERENCE: 30-21(51499)
| CURRENT FILING DATE: 2002-02-25
| PRIOR APPLICATION NUMBER: 09/737,626
| PRIOR PLING DATE: 2000-12-15
| NUMBER OF SEQ ID NOS: 30
| SOFTWARE PATENTING DATE: 2000-12-15
| SOFTWARE PATENTING NOS: 30
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Pred. No. 1.8e-64;
0; Mismatches 37;
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Best Local Similarity 81.1%;
Matches 489; Conservative
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US-09-737-626A-29/c
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NAME/KEY: promoter
LOCATION: (1)..(1800)
CTHER INFORMATION: y = t/u or c
OTHER INFORMATION: chimeric promoter fusion CaMV and Act8 polynucleotides +
OTHER INFORMATION: tro
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14233 ATAGCCTTTCCTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCCTTTTCTACTGTC 14174
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APPLICANT: Fincher, Karen
APPLICANT: Fincher, Karen
APPLICANT: Fincher, Karen
APPLICANT: Wilkinson, Jacob
ALICANT: Wilkinson, Jacob
TITLE OF INVENTION: NO. 64622881 Plant Expression Constructs
FILE REFERENCE: 38-21(51499)C
CURRENT FILING DATE: 2000-12-15
CURRENT FILING DATE: 1999-12-16
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.0
SEQ ID NO 29
LENGTH: 1800
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ilarity 81.1%; Pred. No. 1.8e-64;
Conservative 0; Mismatches 37
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; Sequence 29, Application US/09737698B
; Patent No. 6462258
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Matches 489; Conserv
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                                                                                                      Gaps
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| Patent No. 6948696|
| Patent No. 6948696|
| GENERAL INFORMATION:
| APPLICANT: Fincher, Karen
| APPLICANT: Wilkinson, Jack
| TITLE OF INVENTION: NO. 6946966| Plant Expression Constructs
| TITLE OF INVENTION: NO. 6946966| Plant Expression Constructs
| CURRENT APPLICATION NUMBER: US/10/427,180
| CURRENT APPLICATION NUMBER: US/09/737,626A
| PRIOR FILING DATE: 2002-02-25
| PRIOR FILING DATE: 2002-02-25
| PRIOR FILING DATE: 2002-12-15
| NUMBER OF SEQ ID NOS: 30
| SOFTWARE: PatentIn version 3.0
                                                                                                    : 77
                                                            DB 3; Length 1800;
                                                                                                    Indels
                                                          Score 379.8; DB 3;
Pred. No. 1.8e-64;
0; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          295 ATTACCCTTTGTTGAAAAGTCTCA-----
                                                              5.0%;
81.1%;
                                                                                Best Local Similarity 81.1
Matches 489; Conservative
; OTHER INFORMATION: tro
US-10-427-169-29
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NAME/KEY: promoter
LOCATION: (1)..(1800)
OTHER INFORMATION: y = t/u or c
OTHER INFORMATION: chimeric promoter fusion CaMV and Act8 polynucleotides + Act8
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US-10-427-169-29/c

Sequence 29, Application US/10427169

Patent No. 6919495

GENERAL INFORMATION:

APPLICANT: Fincher, Karen

APPLICANT: Flasinski, Stanislaw

TITLE OF INVERTION: No. 6919495el Plant Expression Constructs

FILE REFERENCE: 38-21(51499)B

CURRENT FILING DATE: 2003-05-01

PRIOR APPLICATION NUMBER: US/09/737,626

PRIOR APPLICATION NUMBER: 09/737,626

PRIOR APPLICATION NUMBER: 09/737,626

PRIOR APPLICATION NUMBER: 09/737,626

SEQ ID NOS: 30

SOFTWARE: PatentIn version 3.0

SEQ ID NO 29

LENGTH: 1800
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EQ ID NO 30
LENGTH: 1742
TYPE: DNA
ORGANISM: artificial sequence
FRATURE:
NAME/KEY: promoter
LOCATION: (1)..(1742)
OTHER INFORMATION: chimeric promoter fusion CaMV and Act2 polynucleotides +
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US-09-737-626A-30/C
; Sequence 30, Application US/09737626A
; Sequence 30, Application US/09737626A
; Patent No. 6660911
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen
; APPLICANT: Fincher, Karen
; APPLICANT: Wilkinson, Jack
; TITLE OF INVENTION: No. 6660911el Plant Expression Constructs
; TITLE OF INVENTION: No. 6660911el Plant Expression
; FILE REFERENCE: 38-21(51499)B
; CURRENT FILING DATE: 2002-02-25
; CURRENT FILING DATE: 2002-02-25
; FRIOR APPLICATION NUMBER: 09/737,626
                                                                                                                                                            Length 1742;
                                                                                                                                                     Score 379.2; DB 3; Length
Pred. No. 2.4e-64;
n. Mismatches 38; Indels
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                                                                                                                                                              similarity 81.0%;
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APPLICANT: Fincher, Karen
APPLICANT: Fincher, Karen
APPLICANT: Wilkinens
APPLICANT: Wilkinens
TITLE OF INVENTION: No. 6462258el Plant Expression Constructs
FILE REFERENCE: 38-21(51499)C
CURRENT APPLICATION NUMBER: US/09/737,698B
CURRENT FILING DATE: 2000-12-15
PRIOR APPLICATION NUMBER: US 60/171,173
PRIOR FILING DATE: 1999-12-16
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.0
                                                                                                                                  Query Match 5.0%; Score 379.8; DB 3; Length Best Local Similarity 81.1%; Pred. No. 1.8e-64; Matches 489; Conservative 0; Mismatches 37; Indels
                   FEATURE:
NAME/KEY: promoter
LOCATION: (1)..(1800)
OTHER INFORMATION: y = t/u or c
OTHER INFORMATION: chimeric promoter fusion CaMV oTHER INFORMATION: tro
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Patent No. 6462258
    ORGANISM: artificial sequence
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      ; ORGANISM: arti
; FEATURE:
NAME/KOX: pron
; LOCATION: (1).
; OTHER INFORMAT
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OTHER INFORMATION: chimeric promoter fusion CaMV and Act2 polynucleotides
OTHER INFORMATION: tro
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CURRENT APPLICATION NUMBER: US/10/427,169
CURRENT FILING DATE: 2003-05-01
FRIOR APPLICATION NUMBER: US/09/737,626A
FRIOR FILING DATE: 2002-02-25
FRIOR PILING DATE: 2000-12-15
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.0
SEQ ID NO 30
LENGTH: 1742
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NAME/KEY: promoter
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OTHER INFORMATION: chimeric promoter fusion CaMV and Act2 polynucleotides +
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Patent No. 6919495
GENERAL INFORMATION:
APPLICANT: Fincher, Karen
APPLICANT: Flasinski, Stanislaw
APPLICANT: Wilkinson, Jack
TITLE OF INVENTION: No. 6919495el Plant Expression Constructs
FILE REFERENCE: 38-21(51499)B
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                                                                                                                                                                                                                                                           Score 379.2; DB 3;
Pred. No. 2.4e-64;
0; Mismatches 38;
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                 NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.0
SEQ ID NO 30
LENGTH: 1742
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Best Local Similarity 81.0%;
Matches 489; Conservative
 PRIOR FILING DATE: 2000-12-15
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BH753412 SALK 0288 BH212594 SALK 0077 BH171104 SALK 0037 BH619277 SALK 0407

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Database

Perfect score:

Sequence:

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Run on:

Scoring table:

Searched:

HTC 06-FEB-2004

linear

mRNA

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Direct Submission

Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage:
BP 191 91006 EWRY cedex - FRANCE (B-mail: seqref@genoscope.cns.fr
- Web: www.genoscope.cns.fr)
The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out full-length librairies construction: Temple G.
Genoscope members carried out sequencing and annotation: Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.
URGV INRA: Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). Sprime and 3 prime are assembled with Phrap.
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                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTFEB522B04 of Flowers and buds of strain col-0 of Arabidopsis thaliana (thale cress).
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/organism="Arabidopsis thaliana"
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Arabidopsis thaliana (thale cress)
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Direct Submission

Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :

BP 191 91006 BVRX cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen) members carried out
full-length librairies construction : Temple G.
Genoscope members carried out sequencing and annotation : Castelli
V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
Schachter V., Weissenbach J., Salanoubat M.

URGY INRA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis
genome released by MIPS (Munich Information center for Protein
Sequences) : 5 prime and 3 prime are assembled with Phrap.
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Arabidopsis thaliana (thale cress)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; crose eudicotyledons;
rosids; eurosids II; Brassicales; Brassicacea; Arabidopsis.

Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C.,
Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V.,
Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M.
Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
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Arabidopsis thaliana Full-length CDNA Complete sequence from clone GSLTFB532B03 of Flowers and buds of strain col-0 of Arabidopsis
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                         1073 TTTGGGTAATATCAACATAAAACTCAGGAACGAACGAGGAATACACACATCATGGGGAGGTAA
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    /db_xref="taxon:3702"
/clone="GSITFB522B04"
/tissue_type="Flowers and bu/ecotype="flowers and bu/ecotype="folol"
/plasmid="pcMvSpORT_6"
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/gene="At3g55370"
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Direct Submission

Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage:
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out full-length librairies construction : Temple G.
Genoscope members carried out sequencing and annotation: Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.
URGV INRA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
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HTC; GSLT CDNA.

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana (thale cress)

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

E (bases 1 to 1320)

Renard,M., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C., Menard,M., Weissenbach,J. and Salanoubat,M.

Temple,G., Caboche,M., Weissenbach,J., and Salanoubat,M.

Whole Genome Sequence Comparisons and 'Pull-Length' cDNA Sequences:

A Combined Approach to Evaluate and Improve Arabidopsis Genome
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Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTFGGH73ZF02 of Hormone Treated Callus of strain col-0 of Axabidopsis thaliana (thale cress).
BX824803
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                                      TTTGGGTAATATCAACATAAACTCAGGCAGGAACGAGGAATACACATCATGGGGAGGTAA
                                                                                  CAGTICITIGGACCGGTITCACCTCCAACAACTCAACAGGCCATCTCTAAGTACT
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14.7%; Score 1118; DB 4;
Best Local Similarity 92.9%; Pred. No. 1.5e-188;
Matches 1221; Conservative 0; Mismatches 0;
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/mol_type="mRNA"
/db_xref="taxon:3702"
/clone="GSLTFB53ZB03"
/tissue_type="Flowers and bu/ecotype="Col-0"
/plasmid="pcMVSPORT_6"
                                                                                                                          /gene="At3g55370"
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/tissue_type="Hormone Treated Callus"
/ecotype="Col-0"
/plasmid="pCMVSPORT_6"
                                                                                                                              Score 964.8; DB 4;
Pred. No. 2.9e-161;
0; Mismatches 92;
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           /mol_type="mRNA"
/db_xref="taxon:3702"
                                                                                           /gene="At3g55370"
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sequences"
/note="Vector: pDS-Lox; Sequence generated in the course of an Arabidopsis T-DNA tagging program. TAIL-PCR was used to generate sequencing templates that represent A.t. genomic DNA flanking the left border of the pDs-Lox T-DNA insert. PCR products were sequenced directly by using the
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Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Wagnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II, Brassicales; Brassicaceae; Arabidopsis.

(bases 1 to 736)
Woody, S.T., Monson, S.S., Jester, P.J., Austin-Phillips, S.,
Amasino, R.M., Sussman, M.R. and Krysan, P.J.
A New Community Resource for Knocking-Out Small Genes and
Tandemly-puplicated Gene Families and for Mosaic Analysis in
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842 AGAGAATGAGGATCGGGGTAGGGATGGGGTGGAGTGAATAACTTATCAAGAAACTC
                                                                                           902 CTTGGGTAATATCAACATAAACTCAGGCAGGAACGAGGAATAACACATCATGGGAGGAAA
                                                                                                                                                                                                                        962 CAGTICTIGGACC-GITICACCCCCAACAACTCAACAGGCCAICTCICATCCTAAGTACT
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/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/cultivar="Col-O ecotype"
/db_xref="taxon:3702"
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transformants"
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University of Wisconsin-Madison
425 Henry Mall, Madison, WI 53706,
Tel: (608) 262-4640
Email: swoody@facstaff.wisc.edu
Class: TAIL-PCR.
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/note="Vector: pDS-Lox; Sequence generated in the course of an Arabidopsis T-DNA tagging program. TAIL-PCR was used to generate sequencing templates that represent A.t. genomic DNA flanking the left border of the pDs-Lox T-DNA insert. PCR products were sequenced directly by using the p745 primer 5' AACGTCCGCAATGTGTTATTAAGTTGTC 3'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5216 CAGCTATATCCAAAGGCTAATTTTGAGGCTCAAAGGAAAGGTATGGTTATAAAACTATCT 5275
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Woody, S.T., Monson, S.S., Jester, P.J., Austin-Phillips, S., Amasino, R.M., Sussman, M.R. and Krysan, P.J.
A New Community Resource for Knocking-out Small Genes and Tandemly-Duplicated Gene Families and for Mosaic Analysis
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100.0%; Pred. No. 4.3e-116;
ative 0; Mismatches 0;
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transformants"
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425 Henry Mall, Madison, WI 53706,
Tel: (608) 262-4640
Email: swood/@facstaff.wisc.edu
Class: TAIL-PCR.
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/cultivar="Col-O ecotype"
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Arabidopsis thaliana
Bukaryota, Viridiplantaes, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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Pred. No. 9.2e-118;
0; Mismatches 12;
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Contact:

Paz Ares, Costantino, Vittorioso, Davies, Gilmartin, Giraudat, Parcy, Sablowski, Coupland, Martin, Angenent, Baeumlein, Carbonero, Colombo, Tonelli, Engstroem, Droege-Least, Gatz, Kavanagh, Kushnir, Zabeau, Laux, Holdsworth Ruberti, Smeekens, Somssich, Weisshaar, Traas

Bielefeld University, Institute for Genome Research Universiteststrasse 25, D-3394 Bielefeld, Germany

Email: bernd weisshaar@uil-bielefeld.de

MGI: AT3G55370; SeqAnalysis: truncated in 5' at pos 179;

Translation: no full cds detected

AGI: AT3G55370; SeqAnalysis: truncated in 5' at pos 179;

Translation: no full cds detected

Data analysis performed in the frame of REGULATORS (Exploiting inter-species conservation in promoter sequences to identify regulators of reproductive development and physiological performance), a Trilateral Co-Operation in Plant Genomics between Spain (MCY). France (GENOPLANTE) and Germany (GABI) coordinated by G. Coupland (coupland-ad-mpiz-koeln.mpg.de). Authors: Vincent Thareau (IBP-Orsay UMR8618 CNRS-UPS, thareau-ad-ibp.u-psud.fr) and Alain Lecharny (MCKV-Erry UMR INRA-CNRS-UBVE,

Definition of the terms used to describe the quality of the clone: The about 2550 sequences from the clone collection were sorted according to clones and clustered. If more than one contig was formed, the clone was designated 'Contamination'. The contiggs and singletons were blasted against CDS plus pseudogenes from the remaining terms for Sequences from the resulting AGI code is presented if more than 90 percent identity was found. The sequences or contigs for which against all TiGRV5 introns, and matches longer than 50 percent identity are reported as 'intron found'. The remaining terms for Sequences, and matches longer than 50 percent identity are reported as 'intron found' all perfect after pairwise allymment with CDS plus pseudogenes from the TiGRV5 annotation file. The sequences or contigs for which against all TiGRV5 protein sequences was perfected. Parter than 95 percent identity; full good: better than 95 percent
                                                                                                   5335
                                                                                                                                                                                                                                                                                                                                                                                                                                           DR750042 972 bp mRNA linear EST 19-JUL-2005 79-L021445-065-006-G10-SeLB MPIZ-ADIS-065d Arabidopsis thaliana cDNA clone 006-G10, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons, rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Paz-Ares, J., Valencia, A., Costantino, P., Vittorioso, P., Davies, F. Gilmartin, P., Giraudat, J., Parcy, F., Reindl, A., Sablowski, R., Coupland, G., Martin, C., Angenent, G.C., Beeumlein, H., Mock, H.P., Carbonero, P., Colombo, L., Tonelli, C., Engstroem, P., Droege-Laser, W., Gatz, C., Ravanagh, T., Kushnir, S., Zabeau, M., Laux, T., Hordsworth, M., Ruberti, I., Ratcliff, F., Smeekens, S., Somssich, I., Weisshaar, B. and Traas, J.

REGIA, an EU project on functional genomics of transcription factors from Arabidopsis thaliana

Comp. Funct. Genomics 3 (2), 102-108 (2002)
CAGCTATATCCAAAGGCTAATTTTGAGGCTCAAAGGAAAGGTATGGTTATAAAACTATCT
                                                                                                                                      5336 ATTTATGTTTAGAATTTGGTCTTATATATTGGCTATATAGAGGTG 5386
                                                                                                                                                                                                                                                                    Arabidopsis thaliana (thale cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DR750042.1 GI:71035382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 972)
                                            250
                                                                                                                                                                                                                                                                                             670
                                                                                                          5276
                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
DR750042/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMMENT
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/lab host="E. coli DHSalpha"
//lab host="E. coli DHSalpha"
//clone lib="MPIZ-ADIG-065d"
//note="Vector: pDONR201; In the context of the EU-funded project REGIA (CDG-CT11999-00876, coordinator Javier Paz-Ares), a set of transcription factor ORFs was generated. The ORFs were produced in a decentralized way in the labs of the participants. Most of the ORFs were generated by RT-PCR using cDNA from various A. thaliana tissues as a template. Initially, it was planned to use year recombination to move the ORFs from the cloning vectors into target constructs. For this reason, a number of the clones contain 'REGIA tags' (RG_tag1: 5pr-AATTCCCGGGAATC-3pr; RG tag2: 5pr-CATGGCAATTCCCGGGAATC-3pr; During the lifetime of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     project, the GATEWAY system became available and finally all ORFs were transferred into GATEWAY vectors. At the end of the REGIA project, the clones were collected as plasmid DNA. For end-sequencing at the DNA core facility of the MPI of Plant Breeding Research (ADIS; head: Bernd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Weisshaar), the plasmids were re-transformed into DHSalpha, arrayed into 96-well plates and new plasmid DNA was prepared. Re-transformation proved to be difficult because a number of clones displayed poor growth. Data submission has been handled by GabiPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    709
percent of the sequence; no similarity: no hit from BLASTp. Note that the collection contains a few clones for which sequencing was not successful, which could have simple technical reasons.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGTGGAACGTGCTCGGAAAGTCCCATTGCCTGAAGCAGCTCTAAATTGCCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GATGTGACTCAACCAATACTAAGTTCTGTTACTTCAATAACTATAGCCTTACTCAACCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCCATTTCTGCAAAACATGTCGTCGCTATTGGACACGTGGCGGTTCCTTGAGGAATGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCCATTTCTGCAAACATGTCGTCGCTATTGGACACGTGGCGGTTCCTTGAGGAATGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGTTGGAGGAGGCTTTTAGGAGGAACAAGAAGAAGCAAATCCAGATCGAAATCTACGGTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                    Obviously, information about these clones is missing in the submitted data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 688.4; DB 8;
Pred. No. 4.5e-112;
0; Mismatches 1;
                                                                                                                                                       Insert Length: 972 Std Brror: 0.00
Seg primer: SeLB GTAACATCAGAGATTTTGAGACAC.
Location/Qualifiers
                                                                                                                                                                                                                                                                       'organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (http://gabi.rzpd.de)."
                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/ecotype="Columbia"
/db_xref="GABI:1452133"
                                                                                                                                                                                                                                                                                                                                                                                        db_xref="taxon:3702"
clone="006-G10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 89.4 Matches 792; Conservative
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엄 ઠે 요 ò g ઠે 쉽 ઠ 셤 ò 셤 ò 셤 ð

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lecharny-adibb. Unsurenty our inserting deality of the clone:
Definition of the terms used to describe the quality of the clone:
The about 220 sequences from the clone collection were sorted
according to clones and clustered. If more than one contig was
singletons were blasted against COS plus pseudogenes from the
TIGRYS annotation, and matches longer than 50 bp with 95
percent identity was found. The sequences were also blasted
against all TIGRYS introns, and matches longer than 50 bp with 95
percent identity are reported as 'intron found'. The remaining
terms for SeqAnalysis describe the outcome of the evaluation of the
CDS detected after pairwise alignment with CDS plus pseudogenes
from the TIGRYS introle as 'intron found'. The remaining
a full CDS with or without STOP codon was detected, a BLASTp
against all TIGRYS protein sequences was performed. Full perfect:
100 percent identity, full good: better than 95 percent identity
over more than 95 percent of the sequence; partial good: better
than 95 percent identity over less than 95 percent identity
weak similarity: less than 95 percent identity
weak similarity: less than 95 percent identity
weak similarity: less than 95 percent identity
obercent of the sequence; no similarity: no hit from BLASTP.
Note
that the collection contains a few clones for which sequencing was
not successful, which could have simple technical reasons.
Obviously, information about these clones is missing in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone=1006-G10"
//lab host==80.coli DH5alpha"
/clone=11b="WetCree" coordinator Javier
/clone=11b="WPIZ-ADIS-065d"
//note=="Vector: pDONR201; In the context of the EU-funded
project REGIA (QLG-T11999-00076, coordinator Javier
Paz-Ares), a set of transcription factor ORFs was
generated. The ORFs were produced in a decentralized way
in the labs of the participants. Most of the ORFs were
generated by RT-PCR using cDNA from various A. thaliana
tissues as a template. Initially, it was planned to use
yeast recombination to move the ORFs from the cloning
vectors into target constructs. For this reason, a number
of the clones contain 'REGIA tags' (RG tag1:
5pr-AATTCCAGCTCACCAC-3pr; RG tag2:
5pr-AATTCCAGCTCACC-3pr; RG tag2:
5pr-CATGGCATTCCCGGGCATC-3pr). During the lifetime of the
project, the GATEWAY system became available and finally
all ORFs were transferred into GATEWAY vectors. At the end
of the REGIA project, the clones were collected as plasmid
of the Reding Research (ADIS; head: Bernd
Weisshaar), the plasmids were re-transformed into
DH5alpha, arrayed into 96-well plates and new plasmid bNA
was prepared. Re-transformation proved to be difficult
because a number of clones displayed poor growth. Data
submission has been handled by Gabipp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4293 GATGTGACTCAACCAATACTAAGTTCTGTTACTTCAATAACTATAGCCTTACTCAACCTC 4352
(coupland-ad-mpiz-koeln.mpg.de). Authors: Vincent
-Orsay UMR8618 CNRS-UPS, thareau-ad-ibp.u-psud.fr) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73 TGGTGGAACGTGCTCGGATCGCAAAAGTCCCATTGCCTGAAGCAGCTCTAAATTGCCCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGTGGAACGTGCTCGCAAAAGTCCCATTGCCTGAAGCAGCTCTAAATTGCCCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 868;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                  Thareau (IBP-Orsay UMR8618 CNRS-UPS, thareau-
Alain Lecharny (URGV-Evry UMR INRA-CNRS-UEVE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: Sela TCGCGTTAACGCTAGCATGGATCTC.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.9%; Score 672.2; DB 8;
88.8%; Pred. No. 3.5e-109;
ive 0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Arabidopsis thaliana"
/mol_type="mRNA"
/ecoType="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                db_xref="GABI:1452143"
|db_xref="taxon:3702"
|clone="006-G10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (http://gabi.rzpd.de)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Insert Length: 868 Std Error:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .868
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Matches 78
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Bielefeld University, Institute for Genome Research
Universitaetsstrasse 25, D-33594 Bielefeld, Germany
Email: bernd.weisshaar@uni-bielefeld.de
AGI: AT3G55370; SeqAnalysis: truncated in 5' at pos 179;
Translation: no full cas detected
Data analysis performed in the frame of REGULATORS (Exploiting
inter-species conservation in promoter sequences to identify
regulators of reproductive development and physiological
performance), a Trilateral Co-Operation in Plant Genomics between
Spain (MCyT), France (GENOPLANTE) and Germany (GABI) coordinated by
                                                                                                                                                                                      4772
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    (bases 1 to 868)

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REGIA, an EU project on functional genomics of transcription factors from Arabidopsis thaliana

Comp. Funct. Genomics 3 (2), 102-108 (2002)
                                                                                             468 GAACTCAAATAAGCAACATGATAAGTGGTATGAGTTCTAGTGGTGGGATCTTGGATGCAT
                                                                                                                                                                                          GGAGAATACCTCCATCACAACAAGCTCAGCAATTCCCTTTCTTGATCAACACTACCGGAT
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                                                                                                                                                                                                                                                                408 GGAGAATACCTCCATCACAACAAGGCTCAGCAATTCCCTTTCTTGATCAACACTACCGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4893 ATTTTTCTTCAGGCGGGGTTAGCGCCACGCAAACAAGAAATGTGAAGGCGGAAGAGAGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5013 ATATCAACATAAACTCAGGCAGGAACGAGAATACACATCATGGGGAGGTAACAGTTCTT
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Arabidopsis thaliana
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DR749973
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DEFINITION
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AUTHORS
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KEYWORDS
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Atlain Lecharity University our invarious of the quality of the clone: The about 220 sequences from the clone collection were sorted according to clones and clustered. If more than one contig was formed, the clone was designated 'Contamination'. The contigs and singletons were blasted against COB plus pseudogenes from the TIGRYS annotation, and the resulting AGI code is presented if more than 90 percent identity was found. The sequences were also blasted against all TIGRYS introns, and matches longer than 50 bp with 95 percent identity are reported as 'intron found'. The remaining terms for Sequences out come of the evaluation of the CDS detected after pairwise alignment with CDS plus pseudogenes from the TIGRYS annotation file. The sequences or contigs for which a full CDS with or without STOP codon was detected, a BLASTP against all TIGRYS protein sequences was performed. Full perfect: 100 percent identity, full good: better than 95 percent identity, over less than 95 percent of the sequence; partial good: better than 95 percent identity over less than 95 percent of the sequence; partial good: better than 95 percent identity over less than 95 percent of the sequence; partial good: better than 195 percent of the sequence; partial good better that the collection contains a few clones for which sequencing was not smallarity: no hit from BLASTP. Note that the collection contains a few clones for which sequencing which could have simple technical reasons.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                where the contraction of con
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/lab host="No: coli DHSalpha"
/clone_lib="MPIZ-ADIS-065d"
/clone_lib="MPIZ-ADIS-065d"
/note="Westor: pDONRS-01; In the context of the EU-funded project REGIA (GLG-CT11999-00876, coordinator Javier Paz-Ares), a set of transcription factor ORFs was generated. The ORFs were produced in a decentralized way in the labs of the participants. Most of the ORFs were generated by RT-PCR using cDNA from various A. thaliana tissues as a template. Initially, it was planned to use yeast recombination to move the ORFs from the cloning vectors into target constructs. For this reason, a number of the clones contein 'REGIA tags' (RG_tag1:
5pr-AATTCCAGCCACC-3pr; RG tag2:
5pr-CATGGCAATTCCCGGGGATC-3pr). During the lifetime of the
                                                                                                                                                                                                                                                                                                                                                             Paz-Ares, Costantino, Vittorioso, Davies, Gilmartin, Giraudat, Parcy, Sabl
owski, Coupland, Martin, Angenent, Baeumlein, Carbonero, Colombo, Tonelli,
Engstroem, Droege-Laser, Gatz, Kavanagh, Kushnir, Zabeau, Laux, Holdsworth
Carbonero, P., Colombo, L., Tonelli, C., Engstroem, P., Droege-Laser, W., Gatz, C., Kavanagh, T., Kushnir, S., Zabeau, M., Iaux, T., Hordsworth, M., Ruberti, I., Ratcliff, F., Smeekens, S., Somssich, I., Weisshaar, B. and Traas, J.
REGIA, an EU project on functional genomics of transcription factors from Arabidopsis thaliana
Comp. Funct. Genomics 3 (2), 102-108 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Insert Length: 866 Std Error: 0.00
Seg primer: SeLA TCGCGTTAACGCTAGCATGGATCTC.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ruberti, Smeekens, Somssich, Weisshaar, Traas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /ecotype="Columbia"
/db_xref="GABI:1452132"
/db_xref="taxon:3702"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone="006-G10"
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                                                                                                                                                                                                                                                                                       JOURNAL
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79-L021444-065-006-G10-SeLA MPIZ-ADIS-065d Arabidopsis thaliana
CDNA clone 006-G10, mRNA sequence.
DR750041
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             Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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Paz-Ares,J., Valencia,A., Costantino,P., Vittorioso,P., Davies,B.,
Gilmartin,P., Giraudat,J., Parcy,F., Reindl,A., Sablowski,R.,
Coupland,G., Martin,C., Angenent,G.C., Baeumlein,H., Mock,H.P.,
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                                                                                                                                                                                                                                             GCCATTTCTGCAAAACATGTCGTCGCTATTGGACACGTGGCGGTTCCTTGAGGAATGTTC
                                                                                                                                                                                                                                                                                                                                      CTGTTGGAGGAGGCTTTTAGGAGGAACAAGAGAAGCAAATCCAGATCGAAATCTACGGTCG
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project, the GATEWAY system became available and finally all ORFs were transferred into GATEWAY vectors. At the end of the REGIA project, the clones were collected as plasmid DNA. For end-sequencing at the DNA core facility of the MPI of Plant Breeding Research (ADIS, head: Bernd Weisshaar), the plasmids were re-transformed into MPISapha, arrayed into 96-well plates and new plasmid DNA was prepared. Re-transformation proved to be difficult bubmission has been handled by GabipD (http://gabi.rzpd.de)."
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Conservative 0; Mismatches 12;
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Citrus clementina

Citrus clementina

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids II; Sapindales; Rutaceae; Citrus.

I (bases 1 to 733)

Forment, J., Gadea, J., Huerta, L., Abizanda, L., Agusti, J., Alamar, S., Alos, E., Andres, F., Arribas, R., Beltran, J.P., Berbel, A.,

Blazquez, M.A., Brumos, J., Canas, L., Gercos, M.,

Colmenero-Flores, J.M., Coneas, A., Estables, B., Gandia, M.,

Garcia-Martinez, J.L., Gimeno, J., Gisbert, A., Gomez, G.,

Gonzalez-Candelas, L., Granell, A., Guerti, J., Laftente, M.T.,

Madueno, F., Marcos, J.F., Marques, M.C., Martinez, F.,

Martinez-Godoy, M.A., Perez-Valle, J., Pons, C., Rodrigo, I.,

Rodriguez, P.L., Royo, C., Serrano, R., Soler, G., Yidal, Ch., Zacarias, L.

Terol, J., Trenor, M., Weello, L., Vicente, O., Vidal, Ch., Zacarias, L.,

and Conejero, V.
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Genomics Laboratory
Instituto de Biologia Molecular y Celular de Plantas (Universidad
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/lab_host="Escherichia coli"
/lab_host="AbsLeaSub1"
/lotoe="Organ: laaves; Vector: pCR2.1; Subtracted cD1
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Emall: jforment@ibmcp.upv.es.
Location/Qualifiers
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765 GGAACGGTTTCACCTCCAACAACAGGCCATCTCTCATCAA
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/organism="Citrus clementina"
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/cultivar="Clemenules"
/db_xref="taxon:85681"
/clone="C21002G02"
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Salanoubat, M., Choisne, N., Artiguenave, F., Brottier, P., Wincker, P., Unpublished
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Submitted (25-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRX cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr |
Location/Qualifiers
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                                                                      TITGITGAAAAGTCTCAATTGCCCTTTGGTCTTCTGAGACTGTATCTTTGATATTTTTGG
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/mol_type="genomic DNA"
db_Aref="laxon:3702"
/clone="F9G12"
/clone=lib="T08"
/ecotype="Columbia"
/note="end::T7"
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1 (bases 1 to 597)
Walbot, V.
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Contact: Walbot V
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                                                             1 TITATITIGITAAAAGGCAFITITITICTIAACAGAGGAAITITACAICAITCTIAGACTGA
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/culTivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
  Indels
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Various BAC End Sequence Database To Identify Minimal Overlaps for Arabidopsis Genomic Sequencing Unpublished (1997) Contact: Steve Rounsley Department of Eukaryotic Genomics
The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA
Thel: 301 838 0200
Fax: 301 838 0209
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/clone lib="IGF"
/note="Vector: BeloBBCII; Site_1: EcoRI; Site_2: EcoRI;
Produced by Thomas Altmann"
                                           Rounsley, S.D., Kelley, J.M., Field, C.E., Craven, M.B., Adams, M.D. Venter, J.C.
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                                                                                                                                                                                                                                                                                                                                                                       thaliana"
                                                                                                                                                                                                                                                                                                                                                                 /organism="Arabidopsis (/mol_type="genomic DNA"/ecotype="Columbia"
                                                                                                                                                                                                                                                                                                             High quality sequence stop: 486.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:3702"
/clone="F9G12"
                                                                                                                                                                                                                                                      Email: rounsley@tigr.org
Seq primer: M13-21
Class: BAC ends
                                    (bases 1 to 486)
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                            /clone lib= mil9 - RescueMu Grid AA"
/clone lib= mil9 - RescueMu Grid AA"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHi, Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA
was extracted from leaf strips, double digested using
BamHI and BglII, and ligated to form circular plasmids.
DHIOB calls were transformed and then screened on LB
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/lab_host="DH10B"
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363 CTTGCCTCCTCCCAAAGCCTTGGAGATTACAATTCAAGCAACACTGGATTAGATTTGG 422
                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 433)
Rounsley,S.D., Field,C.E., Bass,S., Linher,K., Linher,K.,
Oolden,K., Berry,K., Granger,D., Suh,E., Wible,C., Adams,M.D. and
Venter,J.C.
A BAC End Sequence Database for Identifying Minimal Overlaps in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="hermaphrodite"
/clone llb="IGF"
/note="Vector: BeloBACII; Site_1: BCORI; Site_2: ECORI;
Produced by Thomas Altmann"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A BAC End Sequence Database for Identifying Minimal Overlaps in Arabidopsis Genomic Sequencing. Update 3 Unpublished (1997)
Other_GSS8: F18P18TR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Steve Rounsley
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Fax: 301 838 0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. 433

/organism="Arabidopsis thaliana"

/mol type="genomic DNA"

/mol type="Golumbia"

/db xref="taxon:3702"

/clone="F18P18"
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                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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                                             4651 TGGAACTCAAATAAGCAACATGATAAGTGG
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Location/Qualifiers
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Seg primer: M13-21
Class: BAC ends
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Matches 432; Conservative
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                                                                                                                                                                                                       Spermatophyta; Magnoliophyta; audicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

I (bases I to 453.)

Rounaley,S.D., Suh,B.J., Wible,C., Golden,K., Shatsman,S., Choi,P., Yu,K., Akinretoye,B., Shen,K., Goonasekaram,S., Militscher,J., Adams,M.D. and Venter,J.C.

Adams,M.D. and Venter,J.C.

Arabidopsis Genomic Sequencing. Update 4

Unpublished (1999)

L Unpublished (1999)

Other GSSs: F24R16TR

Contact: Steve Rounsley

Department of Enkaryotic Genomics

The Institute for Genomic Research

712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0208

Email: rounsley@tigr.org
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                         AQ011657 452 bp DNA linear GSS 29-MAY-1998
F24E16TFB IGF Arabidopsis thaliana genomic clone F24E16, genomic
                                                                                                                                                                                                                                                                            Choi, P.,
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                                                                                                                                                  Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                                                                                                                eudicotyledons;
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/note="Vector: BeloBACII; Site_1: EcoRI; Site_2: EcoRI;
Produced by Thomas Altmann"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: rounsley@tigr.org
Seq primer: M13-21
Class: BAC ends
High quality sequence stop: 452.
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/ecotype="Columbia"
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/clone="F24E16"
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Enthartoideae; Oryzae; Oryza
                                                                                                                                                                                5878
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                                                             5818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CL517384 1468 bp DNA linear GSS 02-APR-2004 SAC3E03 Flanking Sequence Tag of Oryza sativa T-DNA insertion lines Oryza sativa (japonica cultivar-group) genomic, genomic survey
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                                                                                      301 ACGAGAATTATGCACCTAAATTCAGACTAATCCCCCAAATTTCAGAATTTATGTATTTT 360
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| mol type="genomic DNA"
| cultivar="Nipponbare"
| db_xref="taxon:39947"
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http://genoplante-info.infobiogen.fr)."
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Class: TDNA tagged.
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                                                                     TGGAATCCGAGGAGGTTTCCCGATATTACCCTTTGTTGAAAAGTCTCAATAGCCCTCTGG
                                                                                                                                                                     TCTTCTGAGACTGTATCTTTGATATTCTTGGAGTAGACGAGAGTGTCGTGCTCCACCATG
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TIGTAGAAGCCATCTTCCTTTTCTACTGTCCTTTTCGATGAAGTGACAGATAGCTGGCCAA
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AL132975.1 GI:6434228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Benes, V., Wurmbach, E., Drzonek, H., Ansorge, W., Mewes, H.W., Lemcke, K., Mayer, K.F.X., Quetier, F. and Salanoubat, M. Unpublished
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join(992. .1181,2134. .3164)
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AK221402 Arabidops
AF155818 Arabidops
AF16591 Tobacco r
AF466991 Tobacco r
AF788908 N-termina
AF737283 C-termina
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
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VERARIAKVPLPEAALNCPRCDSTWTKFCYFNNYSLTOPRHFCKTCRRYWTRGGSLRN
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LPTLPPLOSLGDYNSSNTGLPFGGTQISNMLSGMSSGGGILDAWRIPPSQQAQQPFFL
INTTGLVQSSNALYPLEGGVSATQTRNVKAEENDQDRGRDGDGGVNNLSRNFLGNINI
note="EMBL:AF155818 most likely is not full length,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17259. .18094
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join(17259. .17479,17564. .17699,17867. .18094)
/gene="T22E16.50"
/note="similarity to MtN24, Medicago truncatula,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="ubiquitin-conjugating enzyme UBC3"
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                                                                                      /product="zinc finger protein OBP3"
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                                      herfore N-terminal stretch"
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/gene="T22E16.40"
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|gene="T22E16.40"
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/gene="T22E16.40"
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|gene="T22E16.40"
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|gene="T22E16.40"
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|gene="T22E16.40"
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MPDRNRLPRIIFVCCLLHNIIIDMEDGTLDDQPLSQQHDMNYRQRSCKLADEASSVLR
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/gene="T22E16.20"
/note="strong similarity to synaptic glycoprotein SC2
spliced variant, Homo sapiens, EMBL:AF038958"
                                      note="similarity to predicted proteins, Arabidopsis
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/gene="T22E16.20"
complement(join(3660. .3728,3821. .4575,5038. .5077,
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/gene="T22E16.20"
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/gene="T22E16.20"
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/gene="T22E16.20"
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                                                                AAGATTCCTGTTGCATGAAATGTGTTACTAATAAAAAAACACATGCACATTTCTATAA
                                                                                                               TCCAATAGATGAAGACATTATCACTCAGGTTCAGCTACTTCGAAGCGCAACATATCGACA
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8
     membrane
                                                                                                                                                                                                                                             Score 6131.2;
Pred. No. 0;
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     Prokaryotic
                site AA164-174"
                                                                                                                                                                                                                                             80.9%;
99.9%;
                                                                                                                                                                                                                                                                Similarity 99.9
36; Conservative
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Best Local Simil
Matches 6136;
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TTTGAGGCTCAAAGGAAAGGTATGGGGGGGGGGGGGGGG	FINITION Activation-tagging vector pSKI015, complete sequence. CESSION AF187951
23.28	DEF
4081 ANTENGTROMATINGTEMATING ANTENGTROMATING CHARACTERIC A	GGGGTGTACATTGGTGCTTGTCATGCGAGTTATTGCTGAGGAAGATCAAACCATGCAGCT

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3421 TIGIAGAAGCCAICTICCTTITCTACIGICCTITCGAIGAAGTGACAGAAGGGGCAA
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                                                4141 GCATCTTGAACGATAGCCTTTCCTTTATCGCAATGATGATTTGTAGAAGCCATCTCC
                                                                                                                                   CCCGATATTACCCTTTCTTGAAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCT
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                 GCATCTTGAACGATAGCCTTTCCTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCC
                                                                                                           TITICIACTGTCCTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTT
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/db_xref="G1:6537290"
/db_xref="G1:653729
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                                    Activation-tagging vector pSKI015
Activation-tagging vector pSKI015
other sequences; artificial sequences; vectors.

1 (bases 1 to 10138)
Weigel,D., Ahn,J.H., Blazquez,M.A., Borevitz,J.O.,
Christensen,S.K., Fankhauser,C., Ferrandiz,C., Kardailsky,I.,
Malancharuvil,E.J., Neff,M.M., Nguyen,J.T., Sato,S., Wang,Z.,
Xia,Y., Dixon,R.A., Harrison,M.J., Lamb,C.J., Yanofeky,M.F. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4261 TAGITTCGGATCTAGATATCACATCAATCCACTTGCTTTGAAGACGTGGTTGGAACGTCT
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                                                                                                                                                                                                                                                                                                                                                  Kardailsky, I. and Weigel, D.
Direct Submission
Submitted (In-SEP-1999) Plant Biology Laboratory, The Salk
Submitted for Biological Studies, 10010 N. Torrey Pines Road,
Jolla, CA 92037, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="promotes resistance to glutamine synthetase inhibitors"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18.5%; Score 1402.4; DB 11; Length 10138; ilarity 99.9%; Pred. No. 1.7e-195; Conservative 0; Mismatches 1; Indels 0; G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .10138
/organism="Activation-tagging vector pSKI015"
/mol_type="genomic DNA"
/db_xref="taxon:109189"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2894. .4178
/note="caulfilower mosaic virus 35S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="T7 RNA polymerase promoter"
36. .2204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2830. .2849
/note="T7 RNA polymerase promoter"
                                                                                                                                                                                                                                                   Activation tagging in Arabidopsis
Plant Physiol. 122 (4), 1003-1013 (2000)
10759496
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/product="mannopine synthase"
/note="5' end and promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="dervied from pUC19"
2205. .2662
/note="derived from phage fl"
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/note="T-DNA left border"
complement (8054. .8784)
/product="octopine synthase"
/note="3' end"
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/note="derived from pUC19"
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4270. .4294
/note="T-DNA right border"
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/transl_table=1
GI:6537289
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Weigel,D., Blazquez,M.A., Borevitz,J., Christensen,S.K.,
Fankhauser,C., Ferrandiz,C., Malancharuvil,E.J., Neff,M.M.,
Nguyen,J.T., Sato,S., Xia,Y., Wang,Z., Dixon,R.A., Harrison,M.J.,
Lamb,C.J., Yanofeky,M.F. and Chory,J.
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//note==from cauliflower mosaic virus 35S gene promoter"
4270. -420A + 190A + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 190 + 
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Christensen, S.K., Fankhauser, C., Ferrandiz, C., Kardailsky, I.,
Malancharuvil, E.J., Neff, M.M., Nguyen, J.T., Sato, S., Wang, Z.,
Xia, Y., Dixon, R.A., Harrison, M.J., Lamb, C.J., Yanofsky, M.F. and
Chory, J.
                                                                                                                                                                                                    2941 ATATTCTTGGAGTAGACGAGAGTGTCGTGCTCCACCATGTTGGGGATCCACTAGTTCTAG
                                                                                      GATATTACCCTTTGTIGAAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTG
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Pines Road,
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/organism="Activation tagging vector pSKI074"
/mol type="other DNA"
/db_xref="taxon:112458"
12. .31
/note="from T7 RNA polymerase"
                                                                                                                                                                                                                                                                                                                                                                                                                                            complete sequence
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/function="confers kanamycin resistance"
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8756. .9739
/product="neomycin phosphotransferase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Activation tagging vector pSK1074
Activation tagging vector pSK1074
other sequences; artificial sequences; vectors.
( bases 1 to 10450)
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/note="derived from phage f1"

2663. .2829

/note="derived from pUC19"

2830. .2849

/note="from T7 RNA polymerase"
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Plant Physiol. 122 (4), 1003-1013 (2000)
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/note="derived from pUC19"
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/product="neomycin phosphotransferase"
/protein id="AAF26422.1"
/brotein id="AAF26422.1"
/db.xref="Gi16715466"
/db.xref="Gi16715466"
/db.xref="Gi16715466"
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/db.xref="Gi16715460"
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PVLFVKTDLSGALNELQDEAARLSWLATTGVPCAAVLDVVTEAGRDWLLLGEVPGQDL
LSSHLAPAEKVSIMADAWRRIHTLDPATCPFDHQAKHRIERAFTRMEAGLVDQDDLDE
BHQGLAPALEFARLKARNPDGEDLVVTHGDACLPNIMVENGRFSGFIDCGRLGVADRY
GDIALATRDIAERELGGEWADRFLVLYGIAAPDSQRIAFYRLLDEFF"
/profe="from mannopine synthase"
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                                                                                                                                                                                                                                                                                                                                                 Score 1402.4; DB 11; Length 10450; Pred. No. 1.7e-195;
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                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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llarity 99.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                               Similarity
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/codon_start=1
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AWRIPPSQQAQQFPELINTTGLIPPLGSLGGVSATQTRNVKAEENDQDRGRDG
DGVNNLSRNFLGNININSGRNEEYTSWGGNSSWTGFTSNNSTGHLSF"
An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al. (1998) Plant J. 15:707-720; Seki et al. (2002) Science 296:141-145.

This clone is in a modified pBluescript vector.

Please visit our web site (http://rarge.gsc.riken.jp/) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4645 TTTTGGTGGAACTCAAATAAGCAACATGATAAGTGGTATGAGTTCTAGTGGTGGGGATCTT 4704
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Coganism="Arabidopsis thaliana"
/mol.type="mRNA"
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ecotype="Columbia"
note="common name: thale cress"
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134. .1105
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Large-scale analysis of RIKEN Arabidopsis full-length (RAFL) cDNAs Unpublished

2 (bases 1 to 1457)
S. Totoki, Y., Seki, M., Ishida, J., Nakajima, M., Enju, A., Kamiya, A., Narusaka, M., Shin-i, T., Nakagawa, M., Sakamoto, M., Oishi, K., Kohayashi, M., Toyoda, A., Sakaki, Y., Sakurai, T., Iida, K., Akiyama, K., Satou, M., Toyoda, A., Sakaki, Y., Sakurai, T., Iida, K., Kawai, J., Hayashizaki, Y. and Shinozaki, Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, M., Carninci, P., Carninci, P., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana gene for zinc finger protein OBP3, complete cds, clone: RAFL25-48-C17.

AK221402

AK221402

AK21402

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AUTHORS
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/codon start=1
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WRIPPSGQAQQFPFILINTGLVQSSNALYPLLEGGYSATQTRNVKAERNQDRGRDGG
GVNNLSRNFLGNININSGRNEEYTSWGGNSSWTGFTSNNSTGHLSF" 4164 4224 4284 4344 4404 4464 4644 4524 4584 4704 4764 310 4765 TACCGGATTGGTGCAATCTTCAAACGCGTTATATCCATTACTAGAAGGTAAGGGAGGTGT 4824 130 190 250 370 430 490 550 610 670 70 CCTAGATGTGACTCAACCAATACTTAAGTTCTGTTACTTCAATAACTTATAGCCTTAC SCAAGGGAACCAACATCAGCTAGAATGTGTCACAACTGACCAGAACCCTAATAATTA STAAGGGAACCAACATCAGCTAGAATGTGTCACAACTGACCAGAACCCTAATAATTA IGTTCCTGTTGGAGGAGGCTTTAGGAGGAACAAGAGAAGCAAATCCAGATCGAAATC TTACTCAAACCCTAGCAAGTTTCATAGCTACGGTCAAATCCCGGAGTTTAATTCCAACTT 431 TTACTCAAACCCTAGCAAGTTTCATAGCTACGGTCAAATCCCGGAGTTTAATTCCAACTT GCCCATCTTGCCTCCTCTCCAAAGCCTTGGAGATTACAATTCAAGCAACAACTGGATTAGA GGATGCATGGAGAATACCTCCATCACAAGCTCAGCAATTCCCTTTCTTGATCAACAC GGATGCATGGAGAATACCTCCATCACAAGCTCAGCAATTCCCTTTCTTGATCAACAC TTCAATGGTGGAACGTGCTCGGATCGCAAAAGTCCCATTGCCTGAAGCAGCTCTAAA CCTAGATGTGACTCAACCAATACTAAGTTCTGTTACTTCAATAACTATAGCCTTAC CCTCGCCATTTCTGCAAACATGTCGTCGCTATTGGACACGTGGCGGTTCCTTGAG GCCCATCTTGCCTCCTCCAAAGCCTTGGAGATTACAATTCAAGCAACACTGGATTAGA TTTTGGTGGAACTCAAATAAGCAACATGATAAGTGGTATGAGTTCTAGTGGTGGGATCTT 93; Gaps DB 15; Length 1274; 3; Indels 15.3%; Score 1156.2; DB 15 larity 92.9%; Pred. No. 2.9e-159; Conservative 0; Mismatches 3; 4525 4585 4645 4705 491 611 ò g 8 8 8 g ò 셤 8

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AF155818 123-DEC-1999
Arabidopsis thaliana zinc finger protein OBP3 mRNA, complete cds.
AF155818
AF155818.1 GI:5059397

DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

RESULT 5 AF155818 LOCUS

Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

(bases 1 to 1274)
Kang, H.G. and Singh, K.B.
Characterization of Arabidopsis Dof Transcription Factors, a Novel
Zinc Finger Protein Family in Plants

REFERENCE AUTHORS TITLE

JOURNAL

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9225 GCTITGAAGACGGGTIGGAACGICTICITITICCACGAIGITCCICGIGGGGGGCIC
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     /mol type="other DNA"
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/db xref="taxon:188057"
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1. .1639
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1640. .1708
/note="multiple cloning site region"
1709. .2103
/note="TRV strain ppk20 RNA2 3'-sequence"
                                                                                                                                                                                                                                                                 DB 11; Length 9663;
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note="CaMV 35S promoter from pCASS2"
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98.4%; Pred. No. 3.9e-84;
tive 0; Mismatches 3;
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/note="synthetic sequence"
2155. 8894
/note="gcambia 0390 sequence"
8895. 9663
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                                                                                                                                                     AGAGAATGATCAGGATAGGGATAGGGATGGAGTGAATAACTTATCAAGAAACTT
                                                                                                                                                                                                            TTTGGGTAATATCAACATAAACTCAGGCAGGAACGAGGAATACACATCATGGGGAGGTAA
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                                                                                                 1885 CTTGATGGATTTTTCTTCAGGCGGGTTAGCGCCACGCAAACAAGAAATGTGAAGGCGGA
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                                                                                                                                                                                                                                                                    CAGTICTIGGACCGGTITCACCTCCAACAACTCAACAGGCCATCTCCTAATCTAAGTACT
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1 (bases 1 to 963)
Liu, Y., Schiff, M., Marathe, R. and Dinesh-Kumar, S.P.
Tobacco Rarl, EDS1 and NPR1/NIM1 like genes are required for N-mediated resistance to tobacco mosaic virus
PLant J. 30 (44), 415-429 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yale University, 165
CTTTTTTGIGIGITCATTGAATAATCATCGAATTCIC 1274
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Submitted (08-AUG-2001) MCDB,
New Haven, CT 06520, USA
Location/Qualifiers
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12607 bp DNA circular SYN 02-MAR-2005
C-terminal TAP T-DNA vector pYL436, complete sequence.
AY37283
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A C-ferminal tandem affinity purification (TAP) T-DNA vector pYL436
Unpublished
J (bases 1 to 12607)
Liu, Y. and Dinesh-Kumar, S.P.
Direct Submission
Submitted (28-AUG-2004) MCDB, Yale University, New Haven, CT 06520,
                                                                                                                                                                                                                                                                       CCCTCTGGTCTTCTGAGACTGTATCTTTGATATTCTTGGAGTAGAGGAGTGTCGTGCT 6849
                                                                                                                                                                                                    CTGGGCAATGGAATCCGAGGAGGTTTCCCGATATTACCCTTTGTTGAAAAGTCTCAATAG 6789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C-terminal TAP T-DNA vector pYL436
C-terminal TAP T-DNA vector pYL436
other sequences; artificial sequences; vectors.
I (bases 1 to 12607)
Rubio, V., Shen, Y., Saijo, Y., Liu, Y., Gusmaroli, G.,
Dinesh-Kumar, S.P. and Deng, X.W.
An alternative tandem affinity purification strategy applied to Arabidopsis protein complex isolation
Plant J. 41 (5), 767-778 (2005)
211 GATGGCATTTGTAGAGCCATCTTCCTTTTCTACTGTCCTTTCGATGAAGTGACAGATAG
                                                                                 GATGGCATTTGTAGAAGCCATCTTCCTTTTCTACTGTCCTTTCGATGAAGTGACAGATAG
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                                                                                                                                                                                                                       CTGGGCAATGGAATCCGAGGAGGTTTCCCGATATTACCCTTTGTTGAAAGTCTCAATAG
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/organisme"C-terminal TAP T-DNA vector pYL436"
/or_type="cther DNA"
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/note="attR1-CmR-ccdB-attR2 GATEWAY cassette"
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/note="duplicated CaMV 35S promoter"
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/note="protease 3C cleavage site"
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/note="2x 1gG binding domain"
3670. .3932
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3163. .3180
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               A circular SYN 02-MAR-2005 complete sequence.
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Location/Qualifiers
1. .12537
/organism="N-terminal TAPA T-DNA vector pN-TAPA"
/mol_type="cther DNA"
/db_xrefe="texon:300483"
/note="derived from pPZP222"
1. .769
/note="duplicated CaMV 35S promoter"
                                                                                            N-terminal TAPa T-DNA vector pN-TAPa
N-terminal TAPa T-DNA vector pN-TAPa
Other sequences; artificial sequences; vectors.
1 (basea 1 to 12537)
Rubio, V., Shen, Y., Saijo, Y., Liu, Y., Gusmaroli, G.,
Dinesh-Kumar, S.P. and Deng, X.W.
An alternative tandem affinity purification strategy applied to Arabidopsis protein complex isolation
Plant J. 41 (S), 767-778 (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               683 AGATATCACATCAATCCACTTGCTTTGAAGACGTGGGTTGGAACGTCTTTTTTCCACGA
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/note="9x myc tag"

1704. .3577

/note="attR1-CmR-ccdB-attR2 GATEWAY cassette"

/note="NOS terminator"
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/note="TWV U1 omega sequence"
854. .1231
1256. .1279
/note="protease 3C cleavage site"
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Best Local Similarity 98.4%; Pred. No. 3.6e-84;
Matches 660; Conservative 0; Mismatches 3;
                 DNA
                 AY788908 12537 bp DNA
N-terminal TAPa T-DNA vector pN-TAPa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .286. .1303
/note="6x HIS tag"
                                                 AY788908
AY788908.1 GI:55824365
                                                                                                                                                                                                                                                                    2 (bases 1 to 12537)
Rubio, V. and Deng, X.W.
Direct Submission
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CVUI0488 8626 bp DNA circular SYN 28-JAN-1995
Binary cloning vector pPZP121 for plant transformation, complete
sequence.
U10488 U10488.1 GI:506683
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Cloning vector pPZP121
other sequences; artificial sequences; vectors.
I (bases 1 to 0826)
Hajdukiewicz, P., Svab, Z. and Maliga, P.
The small, versatile pPZP family of Agrobacterium binary vectors
for plant transformation
Plant Mol. Biol. 25 (6), 989-994 (1994)
2 (bases 1 to 8626)
                                                                                                                                                                                                                                                                                                                                                                                                                        ATAGCTGGGCAATGGAATCCGAGGAGGTTTCCCGATATTACCCTTTGTTGAAAAGTCTCA
                                                                                                                                                                                                                                                                              AGTAGACGAGAGTGTCGTGCTCCACCATGTTGGGGATCT----AGATATCACATCA
                                                                                                                                                                                                                                                                                                                       CAATGATGGCATTTGTAGAAGCCATCTTCCTTTCTACTGTCCTTTCGATGAAGTGACAG
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                                      Gaps
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                                                           6868 AGATATCACATCACTCACTTGAAGACGTGGTTGGAACGTCT
                                       Indels
                  Length
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                   9
                  Score 621; DB 6;
Pred. No. 3e-81;
0; Mismatches
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                  8.2%;
                                         Conservative
                             Best Local Similarity
Matches 653; Conserv
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                                                                TTTCCACGA
                                                                            TGTTCCTCGTGGGTGGGCGTCCATCTTTGGGACCACTGTCGGTAGAGGCATCTTGAACGA
                                                                                                                     TAGCCTTTCCTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCCTATTTCTACTGTCC
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                                                                                                                                                                                                           TTTGTTGAAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTGATATTCTTGG
                                                                                                                                                                                                                                                                                    AGTAGACGAGAGTGTCGTCCACCATGTTGGGGATCTAGATATCACATCAATCCACTT
                                                                                                                                                                                                                                                                                                                              Gaps
                    Length 12607,
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1 (bases 1 to 5033)

McMullen, M.D., Roth, B.A. and Townsend, R.
Maize chlorotic dwarf virus and resistance thereto
Patent: US 5569828-A 1 29-OCT-1996;

Location/Qualifiers
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                                            Indels
                                                                6190 AGATATCACATCAATCCACTTGCTTTGAAGACGTGGTTGGAACGTCT
                     DB 11;
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                   Score 640.2; DB 1.
Pred. No. 3.6e-84;
0; Mismatches 3
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/wol_type="unassigned DNA'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5033 bp
Sequence 1 from patent US 5569828.
128266
128266.1 GI:1819042
                     Best Local Similarity 98.4%;
Matches 660; Conservative
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Binary cloning vector pPZP221 for plant transformation, complete Bequence.
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Direct Submission

Submitted (09-JUN-1994) Peter Hajdukiewicz, Waksman Institute,
Submitted (09-JUN-1994) Old Hoes Lane, Piscataway, NJ 08855, USA

Location/Qualifiers
                                                                                                                                  Gaps
                                                                                                                                 12;
                                                                                                            Length 8626,
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                                                                                                             DB 11;
                                                           pPZP121
                                                                                                                                  33;
                                                                                                             Score 617.2; DB 1.
Pred. No. 9.2e-81;
0; Mismatches 33
                                                           /organism="Cloning vector
/mol_type="genomic DNA"
/db xref="taxon:35364"
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Best Local Similarity 93.6%;
Matches 659; Conservative (
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                                                                                                                                                                                   2 (bases 1 to 8731)
Hajdukiewicz, P.
Direct Submission
Submitted (09-JUN-1994) Peter Hajdukiewicz, Waksman Institute,
Rutgers University, Old Hoes Lane, Piscataway, NJ 08855, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGATATCACATCAATCCACTTGCTTTGAAGACGTGGGTTGGAACGTCTTCTTTTTCCACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
cloning vector pPZP221

other sequences; artificial sequences; vectors.

(base 1 to 8731)

Hajdukiewicz, P., Svab, Z. and Maliga, P.

The small, versatile pPZP family of Agrobacterium binary for plant transformation
Plant Mol. Biol. 25 (6), 989-994 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
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    .8731
/organisma="Cloning vector pPZP221"
/nol_type="genomic DNA"
/db_xref="texon:35371"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.1%; Score 617.2; DB 1.
larity 93.6%; Pred. No. 9.1e-81;
Conservative 0; Mismatches 33.
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Matches 659;
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/codon_start=1
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/product="Lacz alpha fragment"
/product="Lacz alpha fragment"
/product="Lacz alpha fragment"
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/db_xref="d1:7638146"
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RLAAHPPFASRNNSEBARTDRPSQQLRSLNGEC"
8158. 8414
/note="MUG18 MCS; polylinker"
8656. 8681
/note="right border T-DNA repeat"
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complement(7334. .8114)
/note="CaMV35S2; CaMV 35S promoter, duplicated"
                                                                                                                                                                                                                                                                                                                                                              Length 8742;
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                                                                                                                                                                                                                                                                                                                                                           Score 617.2; DB 1 Pred. No. 9.1e-81;
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93.6%; Pred. No. yor.
'.. 0; Mismatches
                                            3262. .8316
/note="PlacZ; lacZ promoter"
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Matches 659; Conserv
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AF234313
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Roberts, C., Rajagopal, S., Smith, L.M., Nguyen, T.A., Yang, W.,
Rugrohu, S., Ravi, K.S., Vijayachandra, K., Harcourt, R.L.,
Dransfield, L., Desamero, N., Slamet, I., Hadjukiewicz, P., Svab, Z.,
Maliga, P., Mayer, J.E., Kesse, P.K., Kilian, A. and Jefferson, R.A.
A compehensive set of modular vectors for advanced manipulations
and efficient transformation of plants
L. Unpublished
L. Full description of constructs
S. (bases I to 8742)
S. Smith, L.M., Nguyen, T.A., Yang, W.,
Nugrohu, S., Ravi, K.S., Vijayachandra, K., Harcourt, L.,
Dransfield, L., Desamero, N., Slamet, I., Hadjukiewicz, P., Svab, Z.,
Maliga, P., Mayer, J.E., Keese, P.K., Kilian, A. and Jefferson, R.A.
Direct Submission
Location/Qualifiers
Location/Qualifiers
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EDTPPKDPRELYDFLKTEKPEEELVFSHGDLGDSNIFVKDGKVSGFIDLGRSGRADKW
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                                            circular SYN 24-APR-2000
                                                                                                                                                                                       other sequences; artificial sequences; vectors.

1 (sites)
Hajdukiewicz, P., Svab, Z. and Maliga, P.
The small, versatile pPZP family of Agrobacterium binary vectors for plant transformation
Plant Mol. Biol. 25 (6), 989-994 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(4383. .4663)
/note="pBR322 origin of replication"
complement(4954. .5748)
/note="aadA (kanamycin resistance) gene amplified from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. 3442

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/mol_type="other DNA"

/db xref="taxon:118407"

complement(980. .1980)

/note="STA region from pVS1 plasmid"

complement(2573. .3573)

/note="pVS1-REP; replication origin from pVS1"

complement(3983. .4243)

/note="pVS1-REP; replication origin from pVS1"

/note="bow, site from pBR322"
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6173. .6198
/note="left border repeat from C58 T-DNA"
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                                                bp DNA ci:
complete sequence
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/note="CaMV 3'UTR (polyA signal)"
complement(6506. .7303)
/note="npt11 (kanamycin resistance)
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                                                              Binary vector pCAMBIA-2300,
AF234315
AF234315.1 GI:7638145
                                                                                                                                                        Binary vector pCAMBIA-2300
Binary vector pCAMBIA-2300
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AUTHORS
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KEYWORDS
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Solves, 8909 bp DNA circular SYN 28-JAN-1995 Binary cloning vector pPZP111 for plant transformation, complete sequence.
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                                                                                                                                                                                                                                                                                                            8808. .8833
/note="right border T-DNA repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 617.2; DB 1. Pred. No. 9.1e-81;
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/note="puci8 MCS; polylinker"
'note="Placz; lacz promoter'
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                                                                                                                                                                                                                                                                                                                                                                                                                                          8.1%;
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Best Local Similarity 93.6
Matches 659; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product = chloramphenicol acetyl transferase"
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                                                                                                                      Binary vector pCAMBIA-2200
Binary vector pCAMBIA-2200
Binary vector pCAMBIA-2200
Locker sequences; artificial sequences; vectors.

1 (sites)
Hajdukiewicz, P., Svab, Z. and Maliga, P.
The small, versatile pPZP family of Agrobacterium binary vectors for plant transformation
Plant Mol. Biol. 25 (6), 989-994 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Full description of constructs

(bases 1 to 8894)

Roberte, C., Rajagopal, S., Smith, L.M., Nguyen, T.A., Yang, W.,

Roberte, C., Rajagopal, S., Smith, L.M., Nguyen, T.A., Yang, W.,

Nugrohu, S., Ravi, K.S., Vijayachandra, K., Harcourt, R.L.,

Dransfield, L., Desamero, N., Slamet, J., Hadjukiewicz, P., Svab, Z.,

Maliga, P., Mayer, J.E., Keese, P.K., Kilian, A. and Jefferson, R.A.

Direct Submission

Submitted (15-FEB-2000) CAMBIA, Clunies Ross St, Black Mountain /

GPO Box 3200, Canberra, ACT 2601, Australia
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complement (1573. .3573)
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complement (4383. .4663)
/note="pBR322 origin of replication"
complement (5138. .5797)
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/note="CaMV 3'UTR (polyA signal)"
complement (6658. .7455)
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|mol_type="other DNA"
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   complete sequence
Binary vector pCAMBIA-2200,
AF234313
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                                                                  AF234313.1 GI:7638136
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                                                                                                                                                                                                                                                                                                                                                                                  Z (Dases 1 to 8958)
Roberts, C., Rajagopal, S., Smith, L.M., Nguyen, T.A., Yang, W.,
Nugrohu, S., Ravi, K.S., Vijayachandra, K., Harcourt, R.L.,
Dransfield, L., Desamero, N., Slamet, I., Hadjukiewicz, P., Svab, Z.,
Maliga, P., Mayer, J.E., Keese, P.K., Kilian, A. and Jefferson, R.A.
A comprehensive set of modular vectors for advanced manipulations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Black Mountain /
                                                                                                                                                                                                                 1 (sites)
Hajdukiewicz, P., Svab, Z. and Maliga, P.
The small, versatile pPZP family of Agrobacterium binary vectors for plant transformation
Plant Mol. Biol. 25 (6), 989-994 (1994)
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3 (bases 1 to 8958)
Roberts, C., Rajagopal, S., Smith, L.M., Nguyen, T.A., Yang, W.,
Nugrohu, S., Ravi, K.S., Vijayachandra, K., Harcourt, R.L.,
Dransfield, L., Desamero, N., Slamet, I., Hadjukiewicz, P., Svab, Z.,
Maliga, P., Mayer, J.E., Keese, P.K., Kilian, A. and Jefferson, R.A.
Submission
GPO Box 3200, Canberra, ACT 2601, Australia
Location/Qualifiers
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/note="STA region from pVS1 plasmid"
/note="STA region from pVS1 plasmid"
/note="pVS1-REP; replication origin from pVS1"
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| mol type="other DNA"
| Ab xref="taxon:118388"
| join(8944. .8958,1. .219)
                                                                                                                                                                                                  Binary vector pCAMBIA-1300
Binary vector pCAMBIA-1300
other sequences; artificial sequences; vectors
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/note="bom site from pBR322"
complement (4767. .5047)
/note="pBR322 origin of replication"
complement (5338. .6132)
                                                                                                                    vector pCAMBIA-1300, complete sequence.
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/product="Lac2 alpha fragment"
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/note="pUC18 MCS; polylinker"
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                                                       other sequences; artificial sequences; vectors.

(bases 1 to 8909)
Hajdukiewicz,P., Svab,Z. and Maliga,P.
The small, versatile pPZP family of Agrobacterium binary vectors for plant transformation
Plant Mol. Biol. 25 (6), 989-994 (1994)
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                                                                                                                                                                                                                          2 (bases 1 to 8909)
Hajdukiewicz, P.
Direct Submission
Submitted (09-UUN-1994) Peter Hajdukiewicz, Waksman Institute,
Rutgers University, Old Hoes Lane, Piscataway, NJ 08855, USA
1. 8909
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Best Local Similarity 93.6%; Pred. No. 9.1e-81;
Matches 659; Conservative 0; Mismatches 33
                                        Cloning vector pPZP111
Cloning vector pPZP111
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    010487.1
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SLVDGRHPDDAAWAQGRCDAIVRSGAGTVGRTQIARRSAAVWTDGCVEVLADSGNRRFS
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                                                                                        /note="hptII (hygromycin resistance) gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 11; Length
/note="left border repeat from C58 T-DNA"
6649. .6857
/note="CaMV 3'UTR (polyA signal)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33; Indels
                                                                                                                                                                                                                                                                                                                                              complement (7934, .8714)
/note="CaMV35S; 35S promoter from CaMV"
8862. .8916
/note="Placz; lacz promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 617.2; DB 1
Pred. No. 9.1e-81;
0; Mismatches 33
                                                                   complement (6873. .7898
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93.6%;
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Best Local Similarity 93.6
Matches 659; Conservative
                        misc_feature
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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1 agctctattaattcaagaga.....gccgccaccgcggtggagct 7580 9993994 Total number of hits satisfying chosen parameters: 4996997 segs, 3332346308 residues OLIGO NUC Gapop 60.0 , Gapext 60.0 Minimum DB seq length: 0 Maximum DB seq length: 200000000 US-10-650-249-1 7580 0 Scoring table: Perfect score: Word size : Sequence: Searched:

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Adl71829 Arabidops	Adl71846 Arabidops	Abg73047 Tomato an	Adv39061 Plant gen	Adv39062 Plant gen	Aaa88401 4X CaMV 3	Adl71845 Arabidops	Ad171848 Arabidops	Adl71847 Arabidops	Ad171840 Arabidops	Ad171843 Arabidops	Adk59804 Plant DNA	Add30377 Plant yie	Adi44304 Plant tra	Abx56844 Arabidops	Abz15758 Arabidops	Adw39084 Binary ve	Aad39450 FMV35S46	n 225VMe7 19178784
	ID	ADL71829	ADL71846	ABQ73047	ADV39061	ADV39062	AAA88401	ADL71845	ADL71848	ADL71847	ADL71840	ADL71843	ADK59804	ADD30377	ADI44304	ABX56844	ABZ15758	ADW39084	AAD39450	AAC87191
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ďP	Query Match	100.0	19.8	18.5	18.0	18.0	17.9	16.3	14.0	14.0	11.7	9.0	7.7	7.7	7.7	7.6	4.9	4.4	4.0	3.0
	Score	7580	1503	1402	1367	1367	1360	1235	1062	1058	888	684	581	581	581	577	368	331	300	299
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Claim 24; SEQ ID NO 1; 53pp; English

Aaz56878 Constitut	Aaa51890 Chimaeric	Adp64406 CaMV 35S	Aan80891 Sequence	Abv75874 Plant vec	Abv75872 Vector pT	Aas17547 Plasmid p	Aaz47491 pB2LR4 pa	Aaz47492 pB2LR5 pa	Aaz47490 pB1LR3 pa	Aaz47489 pB1LR2 pa	Aaz47493 pB12LR6 n	Aaz47493 pB12LR6 n	Aaz47496 pB12LR9 n	Aaz47496 pB12LR9 n	Aaz47494 pB12LR7 n	Aaz47495 pB12LR8 n	Aas17548 Plasmid p	Aat32317 DNA encod	Aaa88402 CaMV 35S	Adl71841 Arabidops	Aaa75458 Nucleotid	Aaf89826 Nucleotid	Aad06306 CMV 35S p	Aaf89817 Nucleotid	Aad06360 CaMV 35S
AAZ56878	AAA51890	2 ADP64406	AAN80891	ABV75874	ABV75872	AAS17547	AAZ47491	AAZ47492	AAZ47490	AAZ47489	AAZ47493	AAZ47493	AAZ47496	AA247496	AAZ47494	AAZ47495	AAS17548	AAT32317	AAA88402	2 ADL71841	AAA75458	AAF89826	AAD06306	AAF89817	AAD06360
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ALIGNMENTS

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New transgenic plant cell, useful in producing plants with altered size and stature and with normal and healthy root growth.
                                                                                                            Transgenic plant; Dof transcription factor; ocs binding factor; plant size; plant stature; root growth; plant; gene; ds; OBF; OBF binding protein; OBF3; SOB1; mouse-ear cress.
                                                                                                                                                                                Location/Qualifiers
4103. .5119
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/transl_except= (pos:4811. .4909, aa:Gly-Gly)
                    ADL71829 standard; DNA; 7580 BP.
                                                                                        Arabidopsis thaliana OBP3 DNA.
                                                                                                                                                                                                                                                                                                                           28-AUG-2002; 2002US-0406657P.
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                                                                 20-MAY-2004 (first entry)
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                                                                                                                                                          Arabidopsis thaliana.
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The invention relates to a transgenic plant transformed by a Dof transcription factor, OBF (ocs binding factor) binding protein (OBF3). OBF3 is also known as SOB1. The transgenic plant cell and OBF3 nucleic acid and polypeptides are useful in producing transgenic plants with altered size and stature and with normal and healthy root growth. The present sequence is Arabidopsis thaliana OBF3 DNA.
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                                               2376 A; 1376 C; 1291 G; 2537 T; 0 U; 0 Other;
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Oy 5753 TAACCCACGAGAATTATGCACC Db 1321 TAACCCACGAGAATTATGCACT Oy 5813 TATTTTGCGATTTAATATTTG Db 1381 TATTTTGCGATTTAATATTTTG Oy 5873 CAATGGAATGACTGAACCAT Db 1441 CAATGGAATGACTGAACCAT Oy 5933 ACCAATAGGATGATCATGA Db 1501 ACCAATAGAATGATTGTGAACCATGA	OY 5993 GATATGTCATTTATCTGGATA Db 1561 GATATGTCATTTATCTGGATA OY 6053 ATCTTCTTCTAATACATAG OY 613 ATCTTCTTCTAATACATAG OY 6113 TTCAAACATCATT OY 6113 TTCAAACATCATT Db 1681 TTCAAACATCATT OY 6173 ACTTT 6178 Db 1741 ACTTT 1746	RESULT 3 ABQ73047/C ID ABQ73047 standard; DNA; 10078 XX AC ABQ73047; XX DT 24-SEP-2002 (first entry) XX DE Tomato anthocyanin 1 (ANT1) re XX KW Tomato; ANT1; anthocyanin 1; L KW Gene; de. XX CX SX CX SX CX SX CX	XX XX XX 18-JUL-2002. XX 29-OCT-2001; 2001WO-US050638. XX 30-OCT-2000; 2000US-0244685P. XX YX PA (EXEL-) EXELIXIS PLANT SCI INC XX PI Conners K, Mathews HV, Liu A XX WPI; 2002-557819/59. XX New isolated polynucleotide de PT Anthocyanin 1 phenotype in ple PT Anthocyanin 1 phenotype in ple PT Anthocyanin 1 phenotype in ple PT XX PS Example 1; Page 41-46; 53pp; E XX CC CC CC CC COOlynucleotide can be used fou
GATTACAATTCAAGCAACACTGGATTAGATTTTGGTGGAACTCAAATAAGCAACATGATA AGTGGTATGAGTTCTAGTGGTGGAATTTTGGTGGAAATACCTCCATCACAACAA	421 GALTATTCCAATCAGCTAATGTTTAAGCCCTTGATGGATTTTTCTTCAGGCGGGGTTAGC 480 4916 GCCACGCAAACAACAACAAAGAAATGTGAAGGAGGAAGAATGATCAGGATCAGGGTAGGATGGG 4975		ATATGTA ATATGTA CGAATTC CGAATTC CGAATGT CTAATGT CTAATGT CTACCA AATGTAC AATGTAC AATGTAC AATGTAC AATGTAC AATGTAC
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             or
which is responsible for many red and blue colours in plants. The polynucleotide is useful for modifying e.g. leaf colour, flower colour fruit colour in plants. The present sequence represents the plasmid pAG3202 which is used in an example from the present invention for the generation of plants with an ANTI phenotype by transformation with an activation tagging construct
                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGTGGGGCCATCTTTGGGACCACTGTCGGTAGAGGCATCTTGAACGATAGCCTTTCC
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3050 7498 The invention comprises a plant gene activation vector that contains a hairy-root induction gene and enhancer and/or promoter which can function Novel plant gene active vector comprising hairy-root induction gene, and enhancer and/or promoter that functions in plant, useful for activating plant gene forming hairy root. ATTCTTGGAGTAGACGAGAGTGTCGTGCTCCACCATGTTGGGGGATCCACTAGTTCTAGAG GGGGATCTAGATATCACATCAATCCACTTGCTTTGAAGACGTGGTTGGAACGTCTTCTTT TTCCACGATGTTCCTCGTGGGTGGGGGTCCATCTTTGGGACCACTGTCGGTGGGCATC TTGAACGATAGCCTTTCCTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCCTTTTC 3049 TACTGTCCTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCCCGA TATTACCCTTTGTTGAAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTGAT TATTACCCTTTGTTGAAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATGTTGAT **GGGGATCTAGATATCACATCAATCCACTTGCTTTGAAGACGTGGTTGGAACGTCTTCTTT** TTCCACGATGTTCCTCGTGGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCATC TTGAACGATAGCCTTTCCTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCCTTTTC TACTGTCCTTTCGATGATGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCCCGA **TTCTGAGACTGTATCTTTGATATTCTTGGAGTAGACGAGAGTGTCGTGCTCCACCATGTT** 13 ü sequence pHR-AT ф gene activation vector; genetic analysis; Plant gene activation vector-related DNA Claim 4; SEQ ID NO 13; 54pp; Japanese 7580 2848 BP, CGGCCGCCACCGCGGTGGAGCT DNA; 17511 30-MAY-2003; 2003JP-00153985. 28-MAY-2004; 2004WO-JP007789 entry)

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Query Match
18.0%; Score 1367; D
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1367; Conservative 0; Mismatches
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in a plant. The vector of the invention is useful for analyzing a plant gene. The present DNA sequence is claimed in the invention.
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                                                                                        GGGGATCTAGATATCACATCAATCCACTTGCTTTGAAGACGTGGTTGGAACGTCTTCTTT
TTGAACGATAGCCTTTTCCTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCCTTTTTC
                                                                                                                                                                                                                                                                        TIGAACGATAGCCTTTCCTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCCTTTTCT
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The present sequence is that of a 4X cauliflower mosaic virus (CaMV) 35S enhancer sequence preferred for use in the method of the invention. It includes 4 repeats of 202 bp AluI-BcokV fragments of the 35S enhancer, 129 bp of the CaMV sequence associated with each tandem Alu-BcokV repeat, and an additional 7 bp repeated sequence, which does not appear in the 35S enhancer region of the native CaMV genome. This 4X CaMV 35S enhancer clement can be used in a method for identifying genes associated with a desired trait in a fruit-bearing plant. The method involves: transforming plant cells with an activation tagging vector comprising an element which functions to enhance gene expression and has the ability to integrate into the plant genome in a manner effective to enhance expression of cative plant genes, selecting transformed plant cells, regenerating transformed plant cells to yield mature plants, selecting plants having a contribution of which has been enhanced, and confirming the contribution of the modified expression of each identified gene to the desired trait.

The desired trait may be increased resistance to fungal, bacterial or viral pathogens, insects, modifications in flower size, flower number, clower plants characteristics or increased resistantion of leaves and shape, modified seed number, pattern or distribution of leaves and clower plants characteristics or increased drought, salt and antibiotic conference. Plants having short life cycles are transformed, as
                                                                                                                                                                                                                                                        enhancer"
                                                 not associated with 35S enhancer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying genes associated with a desired trait for isolating and characterizing the genes comprises using an enhancer element which enhances gene expression and stably integrates into the plant genome.
                                                                                                                                                                                                                                                       not associated with 35S
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= "CaMV 35S enhancer AluI-EcoRV fragment"
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bp fragment of the CaMV sequence"
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"CaMV 35S enhancer unit 4"
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                                                                         1240 ATCTTGAACGATAGCCTTTCCTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCCTT
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                                                                                           TATTACCCTTTGTTGAAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTGAT
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TTGAACGATAGCCTTTCCTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCCTTTTC
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Best Local Similarity 100.0%; Pred. No. 0;
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AATTCAGACTAATCCCCCCAAATTTCAGAAATTTATGTATTTTGCGATTTAATATTGTGT
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                                           GTCGAATTTTATGACCAAAGTAAATTAATTATGCCGAATGTACATGCTAATATCGAGTTT
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                                                                                                                                   Transgenic plant; Dof transcription factor; ocs binding factor; plant size; plant stature; root growth; plant; gene; ds; OBF; OBF binding protein; OBP3; SOB1; mouse-ear cress.
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                                                                                                                        Transgenic plant; Dof transcription factor; ocs binding factor; plant size; plant stature; root growth; plant; gene; ds; OBF; OBF binding protein; OBF3; SOB1; mouse-ear cress.
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Best Local Similarity 100.0%; Pred. No. 7e-308;
Matches 1062; Conservative 0; Mismatches 0; Indels 0;
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                                                                                                      Arabidopsis thaliana OBP3 antisense DNA #9
                                                                                                                                                                                                                                                                                                                                                                                         Claim 40; SEQ ID NO 20; 53pp; English.
                                    ADL71848 standard; DNA; 1062 BP
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                                                                                   (first entry)
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                                                                                  841 GTTTAAAGTTACTATGACTTTAATCTGAGTTATTTATCCATTTTTTGCAGCTTTGT
                                                                                                                                                                                                       TGAAAAACTATAATTTAATCTGCAATTCTTGTCAAAGTAGTCACAATTTTTATCTATTTTC
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                              GTTTAAAGTTACTATGACTTTAATCTGAGTTATTTATCCATTTTCTTTTTGCAGCTTTGT
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11.7%; Score 888; DB 12; L
Best Local Similarity 100.0%; Pred. No. 6.8e-256;
Matches 888; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 ACAAAAAGAAATAAAGAGCCTAAGAGAATGATGAAAATTGAAAGAGAAAAAAGAGCATTG
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100.0%; Pred. No. 1.1e-306;
ative 0; Mismatches 0;
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Best Local Similarity 100.
Matches 1058; Conservative
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OBF binding protein; OBP3; SOB1; mouse-
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                   Arabidopsis thaliana
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  ATGGTGGAACGTGCTCGGATCGCAAAAGTCCCATTGCCTGAAGCAGCTCTAAATTGCCCT
           AGATGTGACTCAACCAATACTAAGTTCTGTTACTTCAATAACTATAGCCTTACTCAACCT
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                                                                                                                                                                                                                                     361 TIGCCTCCTCTCCAAAGCCTTGGAGATTACAATTCAAGCAACACTGGATTAGATTTTGGT
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                                                                                                                                                                                                                                                                                                                                       TTGGTGCAATCTTCAAACGCGTTATATCCATTACTAGAAGGTAAGGGAGGTGTTAATCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                    GATCAGGATCGGGGTAGGGATGGGAGTGAATAACTTATCAAGAAACTTTTTGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transgenic plant, Dof transcription factor; ocs binding factor; plant size; plant stature, root growth; plant; gene; ds; OBF;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGGACCGGTTTCACCTCCAACAACTCAACAGGCCATCTCTCTAA
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cell, useful in producing plants with altered size normal and healthy root growth. The invention relates to a transgenic plant transformed by a Dof transcription factor, OBF (ocs binding factor) binding protein (OBP3). OBP3 is also known as SOB1. The transgenic plant cell and OBP3 nucleic acid and polypeptides are useful in producing transgenic plants with altered size and stature and with normal and healthy root growth. The present sequence is Arabidopsis thaliana OBP3 antisense DNA. 301 GCTCAGCAATTCCCTTTCTTGATCAACACTACCGGATTGGTGCAATCTTCAAACGCGTTA 4616 GATTACAATTCAAGCAACACTGGATTAGATTTTGGTGGAACTCAAATAAGCAACATGATA 4676 AGTCCTATGAGTTCTAGTCGTCGGGATCTTGGATGCATGGGAGAATACCTCCATCACAACAA 241 Acregraricactricracregerecenterrecarecarecacanacanacanacana GCTCAGCAATTCCCTTTCTTGATCAACACTACCGGATTGGTGCAATCTTCAAACGCGTTA TATCCATTACTAGAAGGTAAGGGAGGTGTTAATCAAGGTGATTCTCAACAGAAGAGTAGT 361 TATCCATTACTAGAAGGTAAGGAGGGAGTGTTAATCAAGGTGATTCTCAACAGAAGAAGGTAGT GATTATTCCAATCAGCTAATGTTTAAGCCCTTGATGGATTTTTTCTTCAGGCGGGGTTAGC GCCACGCAAACAAGAAATGTGAAGGCGGAAGAGAATGATCAGGATCGGGGTAGGGATGGG 4496 AGTACTTCATCACTTACTTCTCGCCCAAGTTACTCAAACCCTAGCAAGTTTCATAGCTAC GGTCAAATCCCGGGGTTTAATTCCAACTTGCCCATCTTGCCTCCTCTCCAAAGCCTTGGA 4436 AACAAGAAGCAAATCCAGATCGAAATCTACGGTCGTGGTCTCGACTGATAATACTACT Gaps ; 0 Length 684; Sequence 684 BP; 212 A; 145 C; 149 G; 178 T; 0 U; 0 Other; 0; Indels 9.0%; Score 684; DB 12; L 100.0%; Pred. No. 6.2e-195; ative 0; Mismatches 0;

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                                               5095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention comprises DNA sequences which confer an altered metabolic characteristic when they are expressed in a plant. The DNA sequences of the invention are useful for producing plants with an altered metabolic characteristic, such as: altered acid metabolism, alcohol metabolism, fatty acid metabolism, altered acid metabolism, altered acid metabolism, altered among altered plant, altered amino acid metabolism, altered ester metabolism, altered amino acid metabolism, altered ester metabolism, altered station, altered station, oxygenated terpene, or isoprenoid metabolism, altered statio, oxygenated terpene, or isoprenoid metabolism, altered station, hydrocarbon metabolism, ketone or quinone metabolism. The DNA sequences of the invention may be used to provide disease resistance in a plant and gene bluffiling or sexual PCR procedures. The present nucleic acid represents a DNA sequence of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel genes that confer altered metabolic characteristics in Nicotiana benthamiana plants, useful for altering the levels of metabolites e.g. acids, fatty acids, amino acids, carbohydrates, hydrocarbons and sterols.
                                                                                                                                                                                                                                                                                                         Plant DNA sequence which confers altered metabolic characteristic #7187.
                                                                                                                                                                                                                                                                                                                                                                                                                                               quinone metabolism; disease resistance; gene shuffling; sexual PCR; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Miller BA;
AACGAGGAATACACATCATGGGGAGGTAACAGTTCTTGGACCGGTTTCACCTCCAACAAC
                                               AACGAGGAATACACATCATGGGGAGGTAACAGTTCTTGGACCGGTTTCACCTCCAACAAC
                                                                                                                                                                                                                                                                                                                                   altered metabolic characteristic; plant; acid metabolism; alcohol metabolism; fatty acid metabolism; branched fatty acid metabolism; alkaloid metabolism; anno acid metabolism; ester metabolism; glyceride metabolism; phenolic metabolism; carbohydrate metabolism; sterol metabolism; terpene metabolism; isoprenoid metabolism; alkene metabolism; alkyne metabolism; hydrocarbon metabolism; ketone metabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pell RJ;
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Reddy AS, Shukla V, Larrinua I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 645 BP; 186 A; 151 C; 141 G; 167 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 7187; 2576pp; English.
                                                                                                         5119
                                                                                                        TCAACAGGCCATCTCTCATTCTAA
                                                                                                                                      rcaacaggccarcrcrcarrcraa
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(DOWC ) DOW AGROSCIENCES LLC.
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                                                                                                                                                                                                                  645
                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                  standard; DNA;
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Crosley R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-313091/30
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7.7%; Score 581; DB 10; Length 645; 00.0%; Pred. No. 3.7e-164;

100.08;

Query Match Best Local Similarity

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                      ATGGTGGAACGTGCTCGGATCGCAAAAGTCCCATTGCCTGAAGCAGCTCTAAATTGCCCT
                                                                                                                                                                                                                                                                     186 CCTGTTGGAGGAGGCTTTAGGAGGAACAAGAGAAAGCAAATCCAGATCGAAATCTACGGTC
                                                                                                                                                                                                                                                                                                                                             TTGCCTCCTCTCCAAAGCCTTGGAGATTACAATTCAAGCAACACTGGATTAGATTTTGGT
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4232 ATGGTGGAACGTGCTCGGATCGCAAAAGTCCCCATTGCCTGAAGCAGCTCTAAATTGCCCT
                                                                          4292 AGATGTGACTCAACCAATACTAAGTTCTGTTACTTCAATAACTATAGCCTTACTCAACCT
                                                                                                              66 AGATGTGACTCAACCAATACTAAGTTCTGTTACTTCAATAACTATAGCCTTACTCAACCT
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A, Pineda O,
                                                                                                                                                      CGCCATTTCTGCAAACATGTCGTCGCTATTGGACACGTGGCGGTTCCT
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Reuber TL, Creelman RA,
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19-NOV-2001; 2001US-0336649P.
1DEC-2001; 2001US-0336692P.
14-JUN-2002; 2002US-00171468P.
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Jiang C, Reub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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Pilgrim ML,
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ADI44304 standard; DNA; 795 BP

22-APR-2004 (first entry)

ADI44304;

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                                                                                                                                                                                                                                                                                                                        The invention relates to a number of isolated Arabidopsis thaliana cDNA sequences and their encoded proteins which are especially transcription factor related cDNA's and proteins. The isolated or recombinant plant transcription factor polymuclectides and polymeptides are useful in producing transgenic plants with commercially valuable properties, i.e. modified or altered desirable traits as compared to a reference plant, such as an alteration in a plant growth characteristic, e.g. growth rate, germination rate of seeds, vigor of plants and seedlings, or leaf and flower senescence. Sequence information related to the polymucleotides and polypeptides can also be used in bioinformatic search methods. The transgenic plant is useful for growing a progeny plant from a parent plant. This sequence represents one of the cDNAs of the invention.
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                                                                                                                              New plant transcription factor polynucleotides and polypeptides, useful in producing transgenic plants with commercially valuable properties, such as an alteration in a plant growth characteristic, e.g. growth rate
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7.7%; Score 581; DB 10; Length 795;
Best Local Similarity 100.0%; Pred. No. 3.5e-164;
Matches 581; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 795 BP; 236 A; 180 C; 175 G; 204 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTGGTGCAATCTTCAAACGCGTTATATCCATTACTAGAAGG 4812
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                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 406; 454pp; English.
                                                     2003-248221/24.
                                                                                  P-PSDB; ADD30378
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Broun PE;
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The invention describes a transgenic plant comprising a recombinant polynucleotide of any one of more than 500 nucleotide sequences fully cledined in the specification or its complement. The method of the invention can be used to produced a plant having altered traits such as: enhanced tolerance to abiotic stress; glyphosphate tolerance; hormone sensitivity; disease resistance; sugar sensitivity or late flowering; altered flower structure, change in stem bifurcations, altered branching pattern, reduced apical dominance, reduced trichome density; lack of trichomes; reduced ectopic trichome development; altered trichome tevelopment; increased root growth; increased root hairs; altered seed development; increased root proliferation or cell differentiation; rapid development; altered cell proliferation or cell differentiation; rapid development; created nearure sensecence; increased necrosis; increase in seedling or plant size; decreased plant size; leaf morphology; seed biochemistry; increase in root anthocyanins; increase in plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New transgenic plant comprising a recombinant polynucleotide of any one of more than 500 nucleotide sequences, useful in bioinformatic search
                                                                                                                   transgenic; plant; enhanced tolerance to abiotic stress; glyphosphate tolerance; hormone sensitivity; disease resistance; sugar sensing; flowering; flower structure; stem bifurcation; branching pattern; apical dominance; trichome; stem morphology; root growth; root hair; seed development; cell proliferation; cell differentiation; premature senescence; necrosis; plant size; leaf morphology; seed morphology; seed biochemistry; root anthocyanin; plant anthocyanin; light response; shade avoidance; bioinformatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J, Broun PE;
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Keddie J
                                                                                       Plant transcription factor related polynucleotide #1741.
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Adam LJ, Reuber TL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 2767; 435pp; English.
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Ratcliffe O, ?
Dubell AN, Pine
                                                                                                                                                                                                                                                         transcription factor; ds
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RIECHMANN J L.
JIANG C.
HEARD J E.
HAAKE V.
CREELMAN R A.
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ADAM L J.
REUBER T L.
KEDDIE J.
BROUN P E.
PILGRIM M L.
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PINEDA O.
YU G.
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Creelman RA,
Pilgrim ML, D
                                                                                                                                                                                                                                                                                       Unidentified.
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LEDPORD B L.
WOESSNER J P.
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KRICKER M. SLATER T.

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DAVIS K FALLEN K.

HOFFMAN N.

AN Y. HAMILTON C M.

GORLACH J.

PRICE J L. RAINES T M. RAMEAKA J G. PAGE A. MATHEW A V.

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27-JAN-2000; 2000US-0178503P
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                                                                                                                                                                    AGATGTGACTCAACCAATACTAAGTTCTGTTACTTCAATAACTATAGCCTTACTCAACCT
                                                                                                                                                                                          AGATGTGACTCAACCAATACTAAGTTCTGTTACTTCAATAACTATAGCCTTACTCAACCT
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  _{\mathrm{The}}
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                                                                                                   Gaps
anthocyanins, or alteration in light response or shade avoidance. Transgenic plant, polymucleotides and polypeptides are useful in bioinformatic search methods. This sequence represents a plant transcription factor related polymucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thale cress, gene; ds; genetic manipulation; plant; blosynthesis; genetic modification; environmental stress; disease resistance; fungicide; insecticide; stress tolerance.
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                                                                             Length 795;
                                                       Sequence 795 BP; 236 A; 180 C; 175 G; 204 T; 0 U; 0 Other;
                                                                           Query Match 7.7%; Score 581; DB 12; Length 7 Best Local Similarity 100.0%; Pred. No. 3.5e-164; Matches 581; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIGGIGCAAICTICAAACGCGTTATATCCATTACTAGAAGG 4812
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                                                                                        Best Local Similarity 100.
Matches 581; Conservative
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The invention relates to Arabidopsis thaliana nucleic acid sequences. The DNA sequences and the polypeptides they encode are useful for identifying Compositions that modulate the homologous or related genes, for producing compositions that modulate the expression or function of the polypeptides, for mapping functional compositions that modulate the physiological pathways, for genetic manipulation of cells, preferably plant cells, in screening assays (avarious plant strains to determine the strains that are capable of withstanding a particular disease or convironmental stress, for enhancing or inhibiting production of biosynthetic products in plants and to create genetically modified and transgenic organisms, such as plant cells and plants. Transgenic plants are useful for introducing or improving disease resistance and stress tolerance in plants, screening biologically active agents, such as coreening biologically active agents, such as coreening biologically active agents, such as Sequences ABX56649-ABX57647 represent Arabidopsis thaliana sequence data for this patent cid not form part of the printed specification but was obtained in electronic format directly from USPTO at sequence data for thal
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                                                                                                                                                                                                                                                                                     Novel Arabidopsis thaliana nucleic acid useful for identifying homologous or related genes, and to create genetically modified and transgenic organisms, such as plant cells and plants.
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                                                  Yu Y;
TD. Haas WD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 ACACATCATGGGGAGGTAACAGTTCTTGGACCGGTTTCACCTCCAACAACACACAGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                               Price JL, Raines TM, Yu Y;
Ledford BL, Woessner JP, Haas I
Davis KR, Allen K, Hoffman N;
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Pred. No. 5.9e-163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Preα. ....
'''A 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 196; 45pp; English.
                                                                         kameaka JG, Page A, Mathew AV,
Garcia CA, Kricker M, Slater T,
Hurban P;
                                                                  Hamilton CM,
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HURBAN P.
                                                            Gorlach J, 1
Rameaka JG,
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Run on:

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AX044091 Sequence
AX036717 Sequence
AX026717 Sequence
A0521 pRT100 DNA
X05868 Plasmid pRT
AR575401 Sequence
BD209862 Improved
BD209861 Improved
BD209861 Improved
BD209864 Improved
BD209864 Improved
BD209864 Improved
BD209864 Improved
BD209864 Improved
BD209864 Improved
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By Arabidopsis and Prancis of PRG, B-mail:

lemcke@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de Project

Coordinator: Marcel Salanoubat and Francis Quelier, Groupement

Goston Cremieux, BP191, 91006 Evry Cedex, France;

http://www.genoscope.cns.fr

Information on performance of analysis and a more detailed

annotation of this entry and other sequences of chromosomes 3, 4

and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/.
                                  CS007934 Sequence
CS025573 Sequence
AJ524488 Arabidops
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryoča, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
AY234328 Binary ve
AY456904 Binary ve
                                                                                       AX405124 Sequence
AR643977 Sequence
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BD209866 Improved
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AX275255 Sequenc
A51131 Sequence
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Lemcke, K., Mayer, K.F.X., Quetier, F. and Salanoubat, M.
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="overlap to BAC T26112 (EMBL:AL132954)"
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join(992. .1181,2134. .3164)
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AR575401
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AF218466 Activatio
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Compugen Ltd.
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                   GenCore version
Copyright (c) 1993 - 2005
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Sequence Sequence

Word size :

Sequence:

Database :

Result Š.

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NWALGKHSRLRK.FPGGKDGKPKYPRRWVILPPFL"
                                                                                                                                                                                                                                                                                                                        DSNGNPLSLNDRVAVALRRLGSGESLSVIGETFGMNQSTVSQITWRFVESMEERAIHH
LSWPSKLDEIKSKFEKISGLPNCCGAIDITHIVMNLPAVEPSNKVWLDGEKNFSMTLQ
AVVDPDMRFLDVIAGWPGSLNDDVVLKNSGFYKLVEKGKRLNGEKLPLSERTELREYI
                                                                                                                                                                                                                                                           /translation="MGPIKTIKKKRAEKKVDRNVLLAATAAATSASAAALNNNDDD
                                                                                                                                                                                                                                                                                                                                                                                                                     VGDSGFPLLPWLLTPYQGKPTSLPQTEFNKRHSEATKAAQMALSKLKDRWRIINGVYM
MPDRNRLPRIIPVCCLLHNIIIDMEDQTLDDQPLSQQHDMYYRQRSCKLADEASSVLR
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/gene="T22E16.20"
/note="strong similarity to synaptic glycoprotein SC2
spliced variant, Homo sapiens, EMBL:AF038958"
                                      note="similarity to predicted proteins, Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8660. .5330
gene="T22E16.20"
complement(join(3660. .3728,3821. .4575,5038. .5077,
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/gene="T22E16.30"
join(10334. .11042,11136. .11350)
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                                                                                                                                                                                                                                 /db_xref="UniProt/TrEMBL:Q9M2U3"
                                                                                                                                /product="putative protein"
/protein_id="CAB75893.1"
/db_xref="GI:7076778"
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site AA164-174"
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Best Local Simi
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4081 AATTAGTACAAATTATGTTAATATGCGAAGGGAACCAACATCAGCTAGAATGTGTCAC 4140		TGCAGGTTCGAGTCAAGCTAGAGTGAATTCAATGGTGGAACGTGCTCGGATCGCAAAAGT	CCCATTCCAAGTCAAGCTACAAGTGAATTCAGTGCAACCTGCTCCGATCGCAAGAAGTTACACTAGCCTTCAACCTAAAGTTTTTTCG 4	TRACTTCAATAACTATAGCCTTACTCAACCTGGCATTTCTGCAAAACATGTCGTCAA	TTGGACACGTGGTTCCTTGAGGAATGTTCCTGTTGGACGAGGCTTTAGGAGGAACAA	GAGAAGCAAATCCAGATCGAAATCTAGGTCGTGGTCTCGACTGATAATACTACTAGTAC 4	TTCATCACTTACTTCTCGCCCAAGTTACTCAAACCCTAGCAAGTTTCATAGCTACGGTCA 4	AATCCCGGAGTTTAATTCCAACTTGCCCATCTTGGCTCCTCTCGAAGCCTTGGAGATTA 4620	CAATTCAAGCAACACTGGATTAGGATTTTGGTGGAACTCAAATAAGCAACATGATAAGTGG 4680 	4740			TTCCAATCAGCTAATGTTTAAGCCCTTGATGGATTTTTCTTCAGGCGGGGTTAGCGCCAC	GCAAACAAGAAATGTGAAGGCGGAAGAGAATGATCAGGATCGGGGTAGGGATGGGGATGG 498	AGTGAATAACTTATCAAGAAACTTTTTGGGTAATATCAACATAAACTCAGGCAGG	5041 GGAATACACATCATGGGGAGGTAACAGTTCTTGGACCGGTTTCACCTCCAACAACTCAAC 5100 UV CACATACACATCATGGGGGAGGTAACAGTTCTTGGACCGGTTTCACCTCCAACAACTCAAC 11331	

TAGCCTTTCCTTTAI	GATATTACCCTTTGTTGAAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTT 396 ATATTCTTGGAGAGAGAGAGTGTCGTGCTCCACCATGTTGGGGATCTAGATATCACA 653 ATATTCTTGGAGTAGAGAGTGTCGTGCTCCACCATGTTGGGGATCTAGATATCACA 653 ATATTCTTGGAGTAGAGAGTGTCGTGCTCCACCATGTTGGGGATCTAGATATCACA 390 CAATCCACTTGGAAGAGTGTGGAACGTCTTTTTTCCACGATGTTCCACG 659	3899 TCAAT 6599 GGGTC 1 3839 GGGTC 6659 TTTAI	CCARTON CONTROL CONT	6839 AGT 3599 AGT 6899 CGT 3539 CGT 6959 ACC 6959 ACC	7019 GTAGAAGCCATCTTTCTACTGTTTTCGATGAGTGACAGATAGTGGGCAATG 7 11111111111111111111111111111111111	Oy 7199 GGGGATCTAGATACAATCCACTTGCTTTGAAGACGTGGTTGGAACGTCTTCTTT 7258
KEYWORDS KEYWORDS Activation-tagging vector pSKI015 ORGANISM Activation-tagging vector pSKI015 ORGANISM Activation-tagging vector pSKI015 ORGANISM Activation-tagging vector pSKI015 OCHES sequences; artificial sequences; vectors. OCHES PAPPING ACTIVATION AND AND AND AND AND AND AND AND AND AN	ad. Ta		362204 /note="dervied from pUC19" 22052662 /note="derived from phage fl" 26632829 /note="derived from pUC19" 28302849 /note="T7 RNA polymerase promoter"	gene promoter enhancer	Anote="promotes resistance to glucamine syntherase inhibitors" /codon_start=1 //trans[rable=1] /protein_id="wak15587.1" /db_xref="G1:637290" /db_xref="G1:637290" /db_xref="G1:637290" /db_xref="g1:637290" /db_xref="mak15587.1" /db_xref="g1:637290" /db_xref="g1:637290" /db_xref="g1:637290" /db_xref="g1:637290" /db_xref="g1:637290" /db_xref="g1:637290" /db_xref="g1:037290" /db_xref="g1:637290" /db_xref="g1:	Query Match 18.5%; Score 1402; DB 11; Length 10138;

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Weigel,D., Blazquez,M.A., Borevitz,J., Christensen,S.K.,
Fankhauser,C., Ferrandiz,C., Malancharuvil,E.J., Neff,M.M.,
Nguyen,J.T., Sato,S., Xia,Y., Wang,Z., Dixon,R.A., Harrison,M.J.,
Lamb,C.J., Yanofsky,M.F. and Chory,J.
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Activation tagging vector pSK1074
other sequences; artificial sequences; vectors.

1 (bases 1 to 10450)
Weigel,D., Ahn,J.H., Blazquez,M.A., Borevitz,J.O.,
Christensen,S.K., Fankhauser,C., Ferrandiz,C., Kardailsky,I.,
Malancharuvil,E.J., Neff,M.M., Nguyen,J.T., Sato,S., Wang,Z.,
Xia,Y., Dixon,R.A., Harrison,M.J., Lamb,C.J., Yanofsky,M.F. and
Activation tagging in Arabidopsis
Plant Physiol. 122 (4), 1003-1013 (2000)
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Submitted (22-DEC-1999) Plant Biology Laboratory, The :
Institute for Biological Studies, 10010 N. Torrey Pine;
Jolla, CA 92037, USA
Location/Qualifiers
1. Organism="Activation tagging vector pSKI074"
//mol_type="other DNA"
//db_xrefe="taxon:112458"
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hote="from cauliflower mosaic virus 35S 4270. .4294

/note="T-DNA right border"
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Droducta-neomycin phosphotransferase"
8771. 9565
/function="confers kanamycin resistance"
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1662. 2205
/note="derived from phage f1"
2663. 2829
/note="derived from pUC19"
2830. 2849
/note="from T7 RNA polymerase"
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/note="from T7 RNA polymerase"
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/podote_t=2inc finger protein OBP3"
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/protein_id="map04355.1"
/db_xref="id1:62320152"
/translation="MYBS2DFWQPDSQWWQQQGWQHQLECVTTDQWPWYLRQLSSP
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AWRIPPSQAQQFPELNTTGLPWGSLGDWSSWTGLDFWGGTQISWMISGMSSGGLLD
PROQAQQFPELNTTGLWQSSWALYPLLEGGWSATQTRAWKREENDQDRGRDG
DGVNNLSRNFLGNININSGRNEEYTSWGGNSSWTGFTSNNSTGHLSF"
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Fax:81-45-503-9586)
An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Sexi et al. (1998) Plant J. 15:707-720; Sexi et al. (2002) Science 296:141-145).
This clone is in a modified pBluescript vector.
Please visit our web site (http://rarge.gsc.riken.jp/) for further
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/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/chromosome="3"
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100.0%; Pred. No. 0;
ative 0; Mismatches 0;
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/note="common name: thale
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134. .1105
/gene="At3g55370"
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Totoki,Y., Seki,M., Ishida,J., Nakajima,M., Enju,A., Kamiya,A.,
Totoki,Y., Seki,M., Ishida,J., Nakagawa,M., Sakamoto,N., Oishi,K.,
Kohara,Y., Kobayshi,M., Toyoda,A., Sakaki,Y., Sakurai,T., Iida,K.,
Akiyama,K., Satou,M., Toyoda,T., Konagaya,A., Carninci,P.,
Kawai,J., Hayashizaki,Y. and Shinozaki,K.
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FLI CDNA.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons, rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
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                                              GTAGAAGCCATCTTCCTTTTCTACTGTCCTTTCGATGAAGTGAGAGAAGAAGCGATG
                                                                                                                     GAATCCGAGGAGTTTCCCCGATATTACCCTTTGTTGAAAAGTCTCAATAGCCCTCTGGTC
                                                                                                                                                 GAATCCGAGGAGGTTTCCCGATATTACCTTTGTTGAAAAGTCTCAATAGCCCTCTGGTC
                                                                                                                                                                                                                              TTCTGAGACTGTATCTTTGATATTCTTGGAGTAGACGAGAGTGTCGTGCTCCACCATGTT
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Qy 4350 CTCGCCATTCTGCAAAACATGTCGTCGTCGTGGCGGTTCCTTGAGGAATG 4409 11	4530 CAAACCCTAGCAGTTTCATAGCTACGGTCAAATCCCGGAGTTTAATTCCAACTTGCCCA 436 CAAACCCTAGCAGTTTCATAGCTACGGTCAAATCCCGGAGTTTAATTCCAACTTGCCCA 436 CAAACCCTAGCAGTTTCATAGCTACGGTCAAATCCCGGAGTTTAATTCCAACTTGCCCA 4590 TCTTGCCTCCTCTCCAAAGCCTTGGAGATTACAATTCAAGCAACACTGGATTAGATTTTG	RESULT 6 AX508868 AX508868 AX508868 AX508868 AX508868 ACESSION AX508868.1 G1:23390105 ANDIGOPSIS thaliana (thale cress) ORGANISM ARADIGOPSIS thaliana (thale cress) AVATHORS BUARTOPA: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Mangoliophyta; eudicotyledons; core eudicotyledons; cosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis. AUTHORS HATPET, J.F., Kreps, J., Wang, X. and Zhu, T. AUTHORS HATPET, J.F., Kreps, J., Wang, X. and Zhu, T. AUTHORS HATPET, J.F., And J.F., And Zhu, T. AUTHORS HATPET, J.F., And	thaliana" DNA" ; DB 6; Length 2000; . 3e-165; CCCAAATTTATGTATTTTGCG	QY 5823 ATTTAATATTGTGTTCACAATCATAATGGCCAACTAACTA
Db 724 TTTTGGTGGAACTCAATAAGCAACATGATAAGTGGTATCTAGTGGGGATCTT 783 Qy 4705 GGATGCATGGAGAATACCTCCATCAACAAGAGAGTGCAATTCTTGATCAACAC 4764 Db 784 GGATGCATGGAGAATACCTCCATCACAACAAGCAATTCCCTTTCTTGATCAACAC 643 Qy 4765 TACCGGATTGGTGCAACTTCAAACGGGTTATATCCATTACTAGAAGG 4812 Db 844 TACCGGATTGGTGCAATCTTCAAACGGGTTATATCCATTACTAGAAGG 891	RESULT 5 AF155818 LOCUS LOCUS LOCUS LOCUS Arabidopsis thaliana zinc finger protein OBP3 mRNA, complete cds. ACCESSION ARPISSB18 ARPISSB18 ARPISSB18 ARPISSB18 ARAbidopsis thaliana (thale cress) SOURCE ARAbidopsis thaliana CRENTOR ARABIGOPSIS thaliana CRESTON ARABIGOPSIS thaliana SOURCE ARABIGOPSIS thaliana Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatrophyta; Magnollophyta; endicotyledons; rosids; eurosids Ito 1274) AUTHORS KANG, H.G. and Singh, K.B. TITLE AUTHORS TITLE Characterization of Arabidopsis Dof Transcription Factors, a Novel JUNUNAL Unpublished AUTHORS KANG, H.G. and Singh, K.B. AUTHORS KANG, H.G. and Singh, K.B.	TITLE Direct Summission JOURNAL Submission JOURNAL Submission JOURNAL Submitted (02-JUN1-1999) MCDB, University of California, Los Angeles, 405 Hilgard Ave., Los Angeles, CA 90095, USA Location/Qualifiers 1. 1274 location/Qualifiers loca	Query Match 9.3%; Score 703; DB 15; Length 1274; Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0; Matches 703; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 4110 AAGGGAACCAACATCAGCTAGAATGTGCACACACACACAC	Db 136 CAATGGGAACGTCGGAATCGCAAAAGTCCCATTGCCTGAAGCTCTAAATTGCC 195 Qy 4290 CTAGATGTGACTCAACCAATACTTAGTTTCTTACTTCAATAACTATAGCCTTACTCAAC 4349 Db 196 CTAGATGTGACTCAACCAATACTAAGTTCTGTTACTTCAATAACTATAGCCTTACTCAAC 255

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Nicotiana tabacum
Nicotiana, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamiids; Solanales; Solanaceae; Nicotiana.
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Submitted (05-DEC-2003) Huang C.Y., School of Molecular & Submitted (05-DEC-2003) Huang C.Y., School of Molecular & Biomedical Science, The University of Adelaide, The University of Adelaide, South Australia, 5005 Adelaide, AUSTRALIA
Location/Qualifiers
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                                                                                                 64 GGTTGGAACGTCTTCTTTTTCCACGATGTTCCTCGTGGGGGGGCCCATCTTTGGGACC
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Simple and complex nuclear loci created by newly transferred chloroplast DNA in tobacco
Proc. Natl. Acad. Sci. U.S.A. 101 (26), 9710-9715 (2004)
15210980
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/note="chloroplast DNA of pPRV111A"
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/organism="Nicotiana tabacum"

/ool_type="genomic DNA"

/cultivar="Petit Havana (N, N)"

/db_xref="taxon:4097"

/note="krl integrant"
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100.0%; Pred. No. 6.4e-148
:ive 0; Mismatches 0;
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780. 1431
/note="neoSTLS2 sequence"
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/note="neoSTLS2 sequence"
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Yamada T., Tanaka, Y. and Kasumi, T.
Yamada, Y. Tanaka, Y. and Kasumi, T.
Putative negative regulator for plant apoptosis
Published Only in DataBase (1999)
2 (bases 1 to 2939)
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiids; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 2939)
       121 ACTGAAACCATGCATAATCTCTCAAGTCTCAACCTATGAAGAATCATGTAACCAATAGAC 180
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/mol_type="genomic DNA"
/cultivar="Bright Yellow"
/db_traxon:4097"
/clone="Tencatively names as S-5"
/cell_type="Suspension cultures"
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Nicotiana tabacum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jakoby,M.J., Heim,M.A. and Weisshaar,B.
Use of a gateway compatible vector for transient plant transfection
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /trānslation="MEKKITGYTTVDISQWHRKEHFEAFQSVAQCTYNQTVQLDITAF
LETYKKNKHKEYPAFHILLARLMNAHPERMAMNGDELVIBOSVHEYTYFHEQTETF
SSIMSEYHDDFRQFHIYSQDVACYGENLAYPPKGFIEMMFFVSANPMVSFTSPDLNV
ANMDNFFAPVFTMGKYYTQGDKVLMPLAIQVHHAVCDGFHVGRMLNELQQYCDEWQGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MQFKVYTYKRESRYRLFVDVQSDIIDTPGRRMVIPLASARLLSD
KVSRELYPVVHIGDESWRMYTTDMASVPVSVIGEEVADLSHRENDIKNAINLMFWGI"
                                                                                                                                                                                                                                                                                                                                                                                  circular SYN 27-MAR-2003
                                             892
                                                                                                                           951 TITCGATGAGAGAGAGAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCCCGATATTACCC
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GERMANY
                                                                                                   6430 TTTGTTGAAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTGATATTTCTTGG
TTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCCCGGATATTACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amp gene; beta lactamase; cat gene; ccdB gene; chloramphenicol acetyl transferase; control of cell death B protein.
Transfection vector pBTdest
Transfection vector pBTdest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jakoby, M.J.

Direct Submission

Submitted (26-MAR-2003) Jakoby M.J., Salamini, MPI for F
Submitted (26-MAR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          product="chloramphenicol acetyl transferase"
protein_id="CAD83080.1"
/db_xref="G1:29335743"
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product="control of cell death B protein"
protein id="CAD83081.1"
db_xref="GI:29335744"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .4462

/organism="Transfection vector pBTdest"

/organism="Transfection vector pBTdest"

/db_xref="taxon:225975"

31. .443

10. te="355"

/note="355"

/note="atkI"

689. .1348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                other sequences; artificial sequences; vectors
                                                                                                                                                                                                   6521
                                                                                                                                                                                                                                                         800
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                                                                                                                                                                                                      6490 AGTAGACGAGAGTGTCGTGCTCCACCATGTTG
                                                                                                                                                                                                                                                                                                                                                                            Transfection vector pBTdest. AJ551314 GI:29335742 amp qene. her.
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/note="attR2"
2168. .2463
/gene="nosT"
2168. .2463
/gene="nosT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  codon_start=1
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/gene="ccdB"
1690. .1995
/gene="ccdB"
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689. .1348
/gene="cat"
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6370
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VFO551314/c
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ACCESSION
VERSION
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AUTHORS
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AUTHORS
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JOURNAL
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/protein_id="CAD83082.1"
/brotein_id="CAD83082.1"
/brotein_id="C1:29335745"
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SPYTEKHLTTOTOMTVRELCSAAITMSDNTAAMLLTTIGGFRELTAFLHNGDHYTRL
DRWEPELNBAIPNDSTTYRVAMATTIRKLITGELITLASRQGLIDWMEADRYARDL
LRSALPAGWFIADKSGAGERGSRGIIAALGPDGKFSRIVVIYTTGSQATWDERNRQIA
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complete
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Submitted (08-AUG-2001) MCDB, Yale University, 165 Prospect Street,
New Haven, CT 06520, USA
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    .9663
/organism="Tobacco rattle virus RNA2-based VIGS vector

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          358 AGATATCACATCAATCCACTTGCTTTGAAGACGTGGTTGGAACGTCTTTTTTCCACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITGITGAAAAGICICAAIAGCCCICTGGICTICTGAGACTGIAICTITGAIAITCITGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    298 TGTTCCTCGTGGGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCATCTTGAACGA
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1 (bases 1 to 9663)
Liu,Y., Schiff,M., Marathe,R. and Dinesh-Kumar,S.P.
Tobacco Ratl, EDS1 and NPR1/NIM1 like genes are required for N-mediated resistance to tobacco mosaic virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                     Length 4462;
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Tobacco rattle virus RNA2-based VIGS vector pTRV2,
Bequence.
                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 100.0%; Pred. No. 5.2e-148; 100.0%; Pred. No. 5.2e-148; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6490 AGTAGACGAGAGTGTCGTGCTCCACCATGTTG 6521
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/product="beta lactamage"
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/db_xref="taxon:188057"
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2606. .3466
/gene="amp"
2606. .3466
/gene="amp"
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C-terminal TAP T-DNA vector pXL436, complete sequence.
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Liu, Y. and Dinesh-Kumar, S.P.
Direct Submission
Submitted (28-AUG-2004) MCDB, Yale University, New Haven, CT 06520,
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  444
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C-terminal TAP T-DNA vector pYL436
other sequences; artificial sequences; vectors.
1 (bases 1 to 1267)
Rubio,V., Shen,Y., Saijo,Y., Liu,Y., Gusmaroli,G.,
Dinesh-Kumar,S.P. and Deng,X.W.
An alternative tandem affinity purification strategy applied that arabidopsis protein complex isolation
Plant J. 41 (5), 767-778 (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 12607)
Liu,Y. and Dinesh-Kumar, S.P.
A C-terminal tandem affinity purification (TAP) T-DNA vector
Unpublished
                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                Length 12537;
                                                                                                                                                                                                                  'note="attR1-CmR-ccdB-attR2 GATEWAY cassette"
                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                              854. .1231
/note=="zx protein A 1gG binding domain"
1265. .1279
/note="protease 3C cleavage site"
             /note="duplicated CaMV 35S promoter"
                                                                                                                                                                                                                                                                                                Query Match
4.4%; Score 332; DB 11; L
Best Local Similarity 100.0%; Pred. No. 4.3e-148;
Matches 332; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    383 AGTAGACGAGAGTGTCGTGCTCCACCATGTTG 352
                               780. .844
/note="TMV Ul omega sequence"
                                                                                                                                                                                                                                   3607. .3863
/note="NOS terminator"
                                                                                                                                                                          /note="9x myc tag"
1704. .3577
                                                                                                                                 1286. .1303
/note="6x HIS tag"
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AY737283.1 GI:52630860
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                                  misc feature
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     promoter
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SOURCE
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AY737283/c
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AUTHORS
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N-terminal TAPa T-DNA vector pN-TAPa, complete sequence.
AY788908
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N-terminal TAPa T-DNA vector pN-TAPa
other sequences; artificial sequences; vectors.
1 (bases 1 to 12537)
Eubio, V., Sen, Y., Saijo, Y., Liu, Y., Gusmaroli, G., Dinesh-Kumar, S.P. and Deng, X.W.
An alternative tandem affainty purification strategy applied tarbaidopsis protein complex isolation
15703063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          To be seen to 12537)

Rubio, V. and Deng, X.W.

Direct Submission

Submitted (21-007-2004) MCDB, Yale University, 165, Prospect

New Haven, CT 06511, USA

Location/Qualifiers
/note="Tobacco rattle virus RNA2-based T-DNA vector synonym: pYL156"
1. .1639
/note="TRV strain ppk20 RNA2 5'-sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="N-terminal TAPa T-DNA vector pN-TAPa"
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0
                                                                                                                                                                                                                                                                  4.4%; Score 332; DB 11; Length 9663;
100.0%; Pred. No. 4.5e-148;
tive 0; Mismatches 0; Indels 0
                                                                   1640. .1708
/note="multiple cloning site region"
1709. .213
/note="TRV strain ppk20 RNA2 3'-sequence"
2104. .2154
/note="synthetic sequence"
2155. .8894
/note="pCambia 0390 sequence"
8895. .9663
/note="CAMV 35S promoter from pCASS2"
                                                                                                                                                                                                                                                                                                                                           6190 AGATATCACATCCACTTGCTTTGAAGACGTGGTTGGAACGTCTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="other DNA"
/db_xref="taxon:300483"
/note="derived from pPZP222"
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Best Local Similarity 100.0
Matches 332; Conservative
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/trānslation="MGPERRPADIRRATEADMPAVCTIVNHYIETSTVNFRTEPQEPQ
EWTDDLVMLAERYFWLVAEVDGEVAGIAYAGPWKARNAYDWTAESTVYVSPHHQRTGL
GSTLYTHLLKSLEAQGFKSVVAVIGLPNDPSVRMHEALGYAPRGMLRAAGFKHGNWHD
VGFWQLDFSLPVPPRPVLPVTEI"
                                                                                                                                                                                                                                                                                                                                                /note="synonym: pat; bialaphos/phosphinothricin resistance gene from Streptomyces hygroscopicus; similar to GenBank Accession Number X17220"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1333. .1935
/note="right border region from nopaline-type Ti plasmid
C58 of Agrobacterium tumefaciens in GenBank Accession
Number X07435."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1231. .1332
/note="multiple cloning site from vector pBlueSfi AB in
GenBank Accession Number AP327874"
                                                                                                                                                  /note="promoter/enhancer sequence from the 35S gene of Cauliflower mosaic virus in GenBank Accession Numbers X05868 and V00140"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1013. .1212
/note="terminator sequence from the 35S gene of
Cauliflower mosaic virus in GenBank Accession Numbers
X05868 and V00140"
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evidence=experimental
replace=""
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/evidence=experimental
/replace="a"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product-"phosphinothricin acetyl transferase"
/protein_id="AAO85365.1"
/db_xref="GI:29569731"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="confers resistance to bialaphos and phosphinothricin"
                                                                                                                                                                                                                                                                                    /note="putative transcription start site"
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1378. .1401
/note="right flanking T-DNA border"
  Geilweilerhof, Siebeldingen 76833, Germany
Location/Qualifiers
                                                            /organism="Binary vector pLH7500"
/mol type="Other DNA"
/db Xref="taxon:226216"
6. 424
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/replace=""
1460..1471
/note=repeat C"
/rpt type=inverted
1485..1495
/note="repeat B"
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/note="repeat C'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="bar"
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392. .398
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Binary vector pLH7500

Binary vector pLH7500

cother sequences; artificial sequences; vectors.

1 (bases 1 to 8903)

Hausmann, L. and Toepfer, R.

Development of Plasmid Vectors

In) Brauer, D., Roebbelen, G. and Toepfer, R. (Eds.);

BIOENGINEERING OF CUSTOM-TAILORED RAPE VARIETIES: 155-172;

GPZ e. V., Von Sieboldstr. 8, Goettingen, Germany (1999)

Hausmann, L. and Toepfer, R.

Direct Submission
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                        1. 12607
/organism="C-terminal TAP T-DNA vector pYL436"
/on_type="other DNA"
/db_xref="taxon:293967"
/note="derived from pPZP222"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.4%; Score 332; DB 11; Length 12607; 100.0%; Pred. No. 4.3e-148; tive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                845. .2718
/note="attR1-CmR-ccdB-attR2 GATEWAY cassette"
                                                                                                                         1...769
/note="duplicated CaMV 35S promoter"
                                                                                                                                                                                                                                                                                                                                                1181. .3204
'note="protease 3C cleavage site"
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                                                                                                                                                                      780. .844
/note≂"TMV Ul omega sequence"
                                                                                                                                                                                                                                                                                                                                                                                           3244. .3591
/note="2x IgG binding domain"
3670. .3932
/note="Nos terminator"
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                                                                                                                                                                                                                                                         2752. .3009
/note="9x myc tag"
3163. .3180
/note="6x HIS tag"
  Location/Qualifiers
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Matches 332; Conservative
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RDWAAVREDQPLTVVGIDRPTIDRDVKAIGRRDFVVIDGAPQAADLAVSAIKAADFVL
IPVQPSPYDIWATADLVELVKQRIEVTDGRLQAAFVVSRAIKGTRIGGEVAEALAGYE
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OIGAALGDDLVEKLKAAQAAQRQRIEAEARPGESWQAAADRIRKESRQPPAAGAPSIR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6430 TITGITGAAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTGATATTCTTGG
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Binary vector pLH7000, complete sequence.
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4.4%; Score 331; DB
Best Local Similarity 100.0%; Pred. No. 1.4
Matches 331; Conservative 0; Mismatches
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/db_xref="G1:29569733"
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/db_xref="GI:29569734"
evidence=experimental
                                                                                                                                                                                                               /codon start=1
/transl_table=11
/product="ParA"
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/transl_table=11
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                      replace="c'
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elidoegrtvkeaaaligvhrstlyralerseevtptearrkgafredalteadalaa
aenerqeeqa"
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3273. .3278
3295. .3295
3095. .3995
/note="resolvase-like protein encoded by park of plasmid
pVS1; similar to Tn3 resolvase in GenBank Accession Number
V00613, Tn917 resolvase in GenBank Accession Number
M1180, and RK2 ParA in GenBank Accession Number
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/note="origin of replication and partitioning region from plasmid pVS1 of Pseudomonas; similar to GenBank Accession Number U10487; serves as origin of replication in Agrobacterium tumefaciens host" /evidence=experimental
                                                                                                                                                                                                                                                            ornithine cyclodeaminase gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="original nucleotide changed to destroy two Sfil restriction sites"
                                                                                                                                                                                                                                                                                                             /note="compared to GenBank Accession Number X07435" /evidence=experimental /replace="t" / replace="t" / replace="t" / note="colin origin of replication sequence of pBR322; similar to GenBank Accession Number J01749; serves as origin of replication in Escherichia coli host"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="original nucleotide changed to destroy a Sfil restriction site"
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1528
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/replace="c"
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/note="compared to GenBank Accession Number J01749"
/revidence=experimental
/replace="gta"
2912
                                                                                                                                                                             to GenBank Accession Number X07435"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="palindromic sequence"
                                                                                                                                                                                                                                    complement (1545. .1935)
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/note="repeat B"
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? 1517
    /rpt_type=inverted
1512. .1522
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                          repeat_region
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-10_signal
RBS_
CDS
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misc_feature
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-10_signal
RBS_
CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="synonym: pat; bialaphos/phosphinothricin resistance
gene from Streptomyces hygroscopicus; similar to GenBank
Accession Number X17220"
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GSTLYFHLLKSLEAGGFKSVVAQVIGLPNDPSVRMHEALGYAPRGMLRAAGFKGNMHD
VGFWQLDFSLPVPPRPVLPVTEI"
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/note="multiple cloning site from vector pBlueSfi BA in
GenBank Accession Number AF327875"
                                                                                                                                                                                                                                                                                                                                                                                                                             Cauliflower mosaic virus in GenBank Accession Numbers X05868 and V00140"
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/note="terminator sequence from the 35S gene of
Cauliflower mosaic virus in GenBank Accession Numbers
X05868 and V00140"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="compared to GenBank Accession Number X17220"
/evidence=experimental
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                                                                                                                             (in) Brauer, D., Roebbelen, G. and Toepfer, R. (Eds.);
BIOENGINEBRING OF CUGTOM-TAILORED RAPE VARIETIES: 155-172;
BIOENGINEBRING OF CUGTOM-TAILORED RAPE VARIETIES: 155-172;
Chases 1 to 8911)
Hausmann, L. and Toepfer, R.

Birct Submission
Submitted (12-FEB-2003) Institute for Grapevine Breeding Geilweilerhof, Sisbeldingen 76833, Germany
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="confers resistance to bialaphos and phosphinothricin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="putative transcription start site"
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Binary vector pLH7000
Binary vector pLH7000
other sequences; artificial sequences; vectors.
( bases 1 to 8911)
Hausmann, L. and Toepfer, R.
Development of Plasmid Vectors
                                                                                                                                                                                                                                                                                                                                  1. .8911
/organism="Binary vector pLH7000"
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1386. .1409
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transl_table=11
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misc_feature
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misc_feature
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                         ORGANISM
                                                               REFERENCE
AUTHORS
                                                                                                             TITLE
JOURNAL
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JOURNAL
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/note="resolvase-like protein encoded by parR of plasmid byS1; similar to Tha resolvase in GenBank Accession Number V00613, Th917 resolvase in GenBank Accession Number MI1180, and RK2 ParA in GenBank Accession Number L27758"
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Tytdrgreilaridhlregdvytvtrldrlarstrldlddartigarghlsilardrd
Tytdrgrentlyrgialafsersellingrregrearkgykrgpretltpaliahar
Eliodgsrtykraallgyhrstyralerseevitptrarrearkbdaltbdala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3124. .6895

Anote—"origin of replication and partitioning region from plasmid pVS1 of Pseudomonas; similar to GenBank Accession Number U10487; serves as origin of replication in Agrobacterium tumefaciens host"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ornithine cyclodeaminase gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="compared to GenBank Accession Number X07435" /evidence=experimental /replace="t" | 1944. .3108 /note="colEl origin of replication sequence of pBR322; similar to GenBank Accession Number J01749; serves as origin of replication in Escherichia coli host" /evidence=experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="original nucleotide changed to destroy a SfiI
                                                                                                                                                                                                                                                                                                                                                                                         ...vee"compared to GenBank Accession Number X07435"
/evidence=experimental
/replace=""
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/note="compared to GenBank Accession Number J01749"
evidence=experimental
                                                                                                                  GenBank Accession Number X07435"
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'note="right flanking T-DNA border"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /widence=experimental
/replace=a,
complement (1553...1943)
/note=13. sequence of the or
ocd; non-functional"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="AAO85361.1"
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1468. 1479
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1439
                                                                                                                  'note="compared to
                                                                                                                                                                                                                                  /rpt_type=inverted
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1520. .1530
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misc_difference 1525
                      1433. .1445
/note="repeat C'"
                                                                                                                                                                                                                                                           (4937. .1503
'note="repeat B"
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|note="repeat B"
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2920
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                                                                                           misc_difference
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                      repeat_region
                                                                                                                                                                                       repeat_region
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QPELASKVDMYMIVGSSVYQBAMNQPGHLRLFVTRIMQEFESDTFFPEIDLGKYKLL
PEYPGVLSEVQBEKGIKYKFEVYEKKD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="synonym: mtx; methotrexate resistance gene from Mus musculus; similar to GenBank Accession Number V00734"
                                                                                                                                             circular SYN 10-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1388. .1990
/note="right border region from nopaline-type Ti plasmid
C58 of Agrobacterium tumefaciens in GenBank Accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence from the 35S gene of
in GenBank Accession Numbers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1060. .1259
/notes-terminator sequence from the 35S gene of
Cauliflower mosaic virus in GenBank Accession Numbers
XOSS68 and V00140"
                                                                                                                                                                                                                                                                                  cother sequences; artificial sequences; vectors.

1 (bases 1 to 8958)

S Haummann, L. and Toepfer, R.
Development of Plasmid Vectors

L (in) Brauer, D., Roebbelen, G. and Toepfer, R. (Eds.);
BIOBNGINEERING OF CUSTOM-TAILORED RAPE VARIETIES: 155-172;
GPZ e. V., VON Sieboldstr. 8, Goettingen, Germany (1999)

E 2 (bases 1 to 8958)
S Hausmann, L. and Toepfer, R.
Direct Submission

L Submitted (12-FEB-2003) Institute for Grapevine Breeding Gellweilerhof, Siebeldingen 76833, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /evidence=experimental
/replace=""
1225. .1240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="multiple cloning site from vector pBlueSfi
GenBank Accession Number AF327875"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="confers resistance to methotrexate"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="putative transcription start site"
439. .1051
/gene="dhfr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="putative transcription stop site"
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/organism="Binary vector pLH5000"
/mol_type="other DNA"
/db xref="taxon:226212"
6. -424
                                                                                                                                         8358 bp DNA Binary vector pLH5000, complete sequence. AY234327
                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="promoter/enhancer
Cauliflower mosaic virus
X05868 and V00140"
      /codon_start=1
/transl_table=11
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/note="multiple
                                                                                                                                                                                                         AY234327.1 GI:29569706
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/gene="dhfr"
                                                                                                                                                                                                                                                   Binary vector pLH5000
Binary vector pLH5000
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TATA_signal
misc_feature
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misc_feature
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                                                                                                                                                                      DEFINITION
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JOURNAL
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AUTHORS
                                                                                                                                                                                                              VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                  AUTHORS
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                                                                                                              RESULT 15
                                                                                                                                                                                           ACCESSION
                                                                                                                                                                                                                                                                                                               REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein id="AAO85362.1"

/db_xref="G1:29569727"

/translation="MKVTAVLAVGGSGKTTIATHLARALQLAGADVLLVUSDPQGSA

RDWAAVREDOPLTVVGIDRPTIDRDVKAIGRRDFVVIDGAPQAADLAVSAIKKADFVL

IPVQESSYDINATADDVELVKQRIEVTDGRLQAAFVVSRAIKGTRIGGEVAEALAGYE

LPILESRITQRVSYPGTAAAGTTVLESEPEGDAAREVQALAABIKSKLI"
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                                                                                                            /note="nucleotide changed to conserve palindromic sequence following Sfil restriction site-destruction" /evidence=experimental /replace="g"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /trānslation="mphywrngrlarrkkrlgclpalqwhwpqargigysgrkpsgpy
oigaalgddlyeklkaaqaaqrqrieaearpgeswqaaadrirkesrqppaagapsir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5258. .6433
/note="partitioning protein ParB encoded by parB of plasmid pVS1; similar to F plasmid SopB in GenBank Accession Number X04619, RKZ KorB in GenBank Accession Number L27758, and Pl ParB in GenBank Accession Number X02954"
                                                                                                                                                                                                                                                                                                                                                                            /note="partitioning protein ParA encoded by parA of plasmid PUSI; similar to F plasmid SoBA in GenBank Accession Number X04619, RKZ IncC in GenBank Accession Number X04619, RKZ incG in GenBank Accession Number L27758, and PI ParA in GenBank Accession Number
                                                                                                                                                                                                   /note="original nucleotide changed to destroy two SfiI restriction sites"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6190 AGATATCACATCAATCCACTTGCTTTGAAGACGTGGTTGGAACGTCTTTTTTCCACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           336 AGATATCACATCAATCCACTTGCTTTGAAGACGTGGTTGGAACGTCTTCTTTTTCCACGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAGCCTTTCCTTTATCGCAATGATGGCATTGTAGAAGCCATCTTCCTTTTCTACTGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCCCGGAATATTACCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5198. .5210
/note="identical to the korB operator binding site of
plasmid RK2 in GenBank Accession Number L27758.1"
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100.0%; Pred. No. 1.4e-147;
rative 0; Mismatches 0; Indels 0
                                                        4147. .4179
/note="palindromic sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="AAO85363.1"
/db_xref="GI:29569728"
                                                                                                                                                                                                                                                     /evidence=experimental
/replace="c"
4237. 4242
4258. 4263
4291. 4298
restriction site"
/evidence=experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       product="ParA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  codon_start=1
transl_table=
                                     replace="c"
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Best Local Similarity
Matches 331; Conserv
                                                                                               misc_difference
                                                                                                                                                                                                 misc_difference
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                                                                                                                                                                                                                                                                                                 -35_signal
-10_signal
RBS
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                                                      stem_loop
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QIGAALGDDIVEKLIKAAQAAQRQRIEREARRPGESWQAADRIRKESRQPPAAGAPSIR
KPPKGDEQPDFFVPMLYDVGTRDSRSIMDVAVFRLSKRDRRAGGVIRYELPOGHVBVS
AGARGAWSWDVDLVLAMVSHLTESMNRYREGKGDRGRVFRPHVADVLKFCRRADGG
KQKDDLVETCIRLATHVAMQRIKKAKNGRLVTVSEGEALISRYKIVKSETGRHEYIE
IELADWMYREITEGKNPDVLTVHPDYFLIDPGIGRFLYRLARRAAGKAEARRLFKTIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /trānslation="MKVIAVINQKGGSGKTTIATHLARALQLAGADVLLVDSDPQGSA
RDWAAVREDQPLTVVGIDRPTIDRDVKAIGRRDFVVIDGAPQAADLAVSAIKAADFVL
IPVQPSPYDIWATADLVELVKQRIEVTDGRLQAAFVVSRAIKGTRIGGEVAEALAGYE
LPILESRITQRVSYPGTAAAGTTVLESEPEGDAAREVQALAABIKSKLI"
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                 DTTTPAGRMVLTVFAGIABFERSLIIDRTRSGRBAAKARGVKFGPRPTLTPAQIAHAR
ELIDQBGRTVKEAAALLGVHRSTLYRALERSBEVTPTEARRRGAFREDALTBADALAA
                                                                                                                                                                                                                                                                                 'note="nucleotide changed to conserve palindromic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translation="MPHVWRNGRLARRKRLGCLPALQWHWNPQARGIGVSGRKPSGPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ERSGSAGEFKKFCFTVRKLIGSNDLPEYDLKEEAGQAGPILVMRYRNLIEGEASAGS"
trrdrpelarmldhlrpgdvvtvtrldrlarstrdllderiqeagaglrslaepwa
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//note="identical to the korB operator binding site of plasmid RK2 in GenBank Accession Number L27758.1"

5305. .6480

//note="partitioning protein ParB encoded by parB of plasmid pVS1, similar to F plasmid SopB in GenBank Accession Number X04619, RK2 KorB in GenBank Accession Number L27758, and Pl ParB in GenBank Accession Number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="partitioning protein ParA encoded by parA of plasmid pVS1; similar to F plasmid SopA in GenBank Accession Number X04619, RKZ IncC in GenBank Accession Number LTT58, and Pl ParA in GenBank Accession Number
                                                                                                                                                                                                                                                                                                                                                                                     /note="original nucleotide changed to destroy two Sfil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6190 AGATATCACATCAATCCACTTGCTTTGAAGACGTGGTTGGAACGTCTTTTTTCCACGA
                                                                                                                /note="original nucleotide changed to destroy a SfiI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="compared to GenBank Accession Number U10487"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                     following SfiI restriction site-destruction"
/evidence=experimental
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                                                                                                                                                                                                               4194. .4226
/note="palindromic sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="AAO85347.1"
/db_xref="GI:29569709"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="AA085348.1"
                                                                                                                                                                 /evidence=experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   /evidence=experimental
                                                                                                                                             restriction site"
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/product="ParB"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon start=1
                                                                                                                                                                                       /replace="c"
                                                                                                                                                                                                                                                                                                                                                        /replace="g"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /replace="c"
4284. .4289
                                                                         AENERQEEQA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . .4345
                                                                                                                                                                                                                                                           misc_difference 4202
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Matches 331;
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-10_signal
RBS_
CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pVS1; similar to Tn3 resolvase in GenBank Accession Number V00613, Tn917 resolvase in GenBank Accession Number M1180, and RK2 ParA in GenBank Accession Number L27758"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MNKSAAAGLLGYARVSTDDQDLTNQRAELHAAGCTKLFSEKITG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3171. .6942
/note="origin of replication and partitioning region from
plasmid pVS1 of Pseudomonas; similar to GenBank Accession
Number U10487; serves as origin of replication in
Agrobacterium tumefaciens host"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="resolvase-like protein encoded by parR of plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ornithine cyclodeaminase gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1991. .1155
/note="ColEI origin of replication sequence of pBR322;
similar to GenBank Accession Number J01749; serves as
origin of replication in Escherichia coli host"
/evidence=experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="compared to GenBank Accession Number J01749"
|evidence=experimental
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/note="compared to GenBank Accession Number J01749"
/evidence=experimental
                                                     'note="compared to GenBank Accession Number X07435"
                                                                                                                                                                                                                                                              GenBank Accession Number X07435"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="compared to GenBank Accession Number X07435"
(evidence=experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="compared to GenBank Accession Number X07435"
/evidence=experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="compared to GenBank Accession Number X07435"
                                                                      /evidence=experimental
/replace="a"
1433. .1456
/note="right flanking T-DNA border"
/note="repeat C'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (1600. .1990)
/note="3' sequence of the ocd; non-functional"
1776
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/db_xref="GI:29569708"
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1540. 1550
/note="repeat B"
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1486
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1567. .1577
/note="repeat B"
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1572
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Search completed: December 31, 2005, 14:03:29 Job time : 24339 secs

111, Appl 12, Appl 12, Appl 31, Appl 30, Appl 5254799 30, Appl 52, Appl 14, Appl 14, Appl 14, Appl 14, Appl 11, Appl 11, Appl 11, Appl 12, Appl 12, Appl 13, Appl 14, Appl 16, Appl 17, Appl 18, Appl 18, Appl 19, Appl 19,

Sequence 1 Sequence 1 Sequence 1 Sequence 3 Sequence 3 Sequence 3

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Sequence:

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Sequence 3,

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6378 AAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCCCGATATTACCCTTTGTTGA 6437
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Sequence 46, Application US/10012070A

Patent No. 6867293

GENERAL INFORMATION:

APPLICANT: Hawkes, Timothy

APPLICANT: Marner, Simon

APPLICANT: Andrews, Christopher

APPLICANT: Bachoo, Satvinder

APPLICANT: Pickerill, Andrew

TITLE OF INVENTION: Herbicide Resistant Plants

TILE REFERENCE: 50490/UST

CURRENT APPLICATION NUMBER: US/10/012,070A

CURRENT PILING DATE: 2001-10-29

PRIOR APPLICATION NUMBER: PCT/GB00/01573

PRIOR APPLICATION NUMBER: PCT/GB00/01573

PRIOR APPLICATION NUMBER: PCT/GB00/01573

PRIOR APPLICATION NUMBER: PCT/GB00/01573

PRIOR PRIOR PLING DATE: 2000-04-20

NUMBER OF SEQ ID NOS: 57
US-09-577-424-1

US-09-056-163-11

US-09-056-163-11

US-08-46-486-31

US-08-46-486-31

US-08-46-486-31

US-08-46-486-30

US-08-46-30-30

US-08-46-30-30

US-09-363-30-30

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US-08-458-093-2

US-08-458-083-10-14

US-08-459-680A-5

US-08-450-814-5

US-08-450-814-5

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Best Local Similarity 100.
Matches 299; Conservative
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                                      GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-353-332-1
US-09-8469-211A-19
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US-09-8469-211A-19
US-09-810-861B-3
US-09-816-402B-7
US-09-328-402B-7
US-09-330-737-1
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Gapop_60.0, Gapext 60.0
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Maximum DB seq length: 200000000
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Match Length DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                257 GTTCCTCGTGGGGGGGGCTCCATTGGGACCACTGTCGGTAGAGGCATCTTGAACGAT
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                                                 Sequence 1, Application US/09353332;
Sequence 1, Application US/09353332;
Patent No. 6316697;
GENERAL INFORMATION:
APPLICANT: Dixon, Richard A.
TITLE OF INVENTION: CONSTITUTIVE DISEASE RESISITANCE (CDR1);
TITLE OF INVENTION: GENE AND METHODS OF USE THEREOF;
TITLE OF INVENTION: GENE AND METHODS OF USE THEREOF;
FILE REFERENCE: SALK2820-1;
CURRENT FILING DATE: 1999-07-14;
EARLIER FILING DATE: 1998-07-14;
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for Windows Version 4.0;
SEQ ID NO 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 3.7%; Score 281; DB 3; Length 4839; Best Local Similarity 100.0%; Pred. No. 3.4e-97; Matches 281; Conservative 0; Mismatches 0; Indels
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APPLICANT: J. Archer
TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN EUKARYOTES
FILE REFERENCE: 9341-021
CURRENT APPLICATION NUMBER: US/09/469,211A
CURRENT FILING DATE: 1999-12-22
PRIOR APPLICATION NUMBER: UK 9828660.2
PRIOR APPLICATION NUMBER: US 9828660.2
NUMBER OF SEQ IN DOS: 19
SOFTWARE: PATENTING DATE: 1998-12-24
NUMBER OF SEQ IN OS: 19
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US-09-469-211A-19/c
; Sequence 19, Application US/09469211A
; Patent No. 6660524
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ORGANISM: Artificial Sequence
FBATURE:
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US-09-353-332-1
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RESULT 2
US-09-353-332-1/c
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LENGTH: 470
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                                                                                                                                                          235 TCTTGAACGATAGCCTTTCCTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCTTT
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US-09-810-861B-3
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; OTHER INFORMATION: Description of Artificial Sequence:chimaeric; ; OTHER INFORMATION: promoter US-09-469-211A-19
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                                                                  Query Match
2.9%; Score 222; DB 3; Length 470;
Best Local Similarity 100.0%; Pred. No. 1.2e-74;
Matches 222; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 7.9e-75;
:ive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 222; Conservative
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456 TCTACTGTCCTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGATTCCC 397
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US-09-042-426-1/C
is Sequence 1, Application US/09042426
; Patent No. 6114608
; GENERAL INFORMATION:
; APPLICANT: ITVIN J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
; TITLE OF INVENTION: DNA CONSTRUCT Containing Bacillus
; TURBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 611460Bartis Corporation
; """" F4 MORTIS Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 2728;
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CITY: 564 Morris Avenue
CITY: Summit
STATE: New Jersey
COUTRY: USA
ZIP: 07901
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,426
FILING DATE: March 13, 1998
CLASSIFICATION: 8000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.9%; Score 221; DB 3; 100.0%; Pred. No. 2.1e-74; tive 0; Mismatches 0;
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 44 40 200.7 (Germany)
APPLICATION NUMBER: 44 40 200.7 (Germany)
FILING DATE: 10-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Kurf G. Briscoe
REGISTAATION NUMBER: 33,141
REFERENCE/DOCKET NUMBER: Bayer 9840-KGB
TELECHONNICATION INFORMATION:
TELECHONE: (914) 332-1844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Hoxie, Thomas
REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8614
                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2728 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA (genomic)
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Best Local Similarity 100.
Matches 221; Conservative
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                                                                               GENERAL INFORMATION:
APPLICANT: Soreq, Hermona
APPLICANT: Soreq, Hermona
APPLICANT: Soreq, Hermona
APPLICANT: Arntzen, Charles J.
APPLICANT: Arntzen, Charles J.
APPLICANT: Arntzen, Charles J.
TITLE OF INVENTION: TRANSGENIC PLANTS
FILE REFERENCE: BTL 45
CURRENT APPLICATION NUMBER: US/09/810,861B
CURRENT FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/190,440
PRIOR FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PATENTIN VEr. 3.1
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature; LOCATION: (11862)..(12157)
. COTATION: (11862)..(12157)
. OTHER INFORMATION: Description of Artificial Sequence: plasmid vector; CHER INFORMATION: pTM036. Identity of sequence residues 11862-12157 unknown. US-09-810-8618-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13991 TCTTGAACGATAGCCTTTCCTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCCTTT 13932
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ZIP: 10.591-5144
COMPUTER READABLE FORM:
MEDIUM TYPE: Disketc, 3.50 inch, 2.0 MB storage COMPUTER: Gateway 2000
OPERATING SYSTEM: DOS
SOFTWARE: Microsoft Windows 98
CURRENT APPLICATION DATE: US/08/836,402B
FILING DATE: 02-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
2.9%; Score 222; DB 3; L
Best Local Similarity 100.0%; Pred. No. 6.7e-75;
Matches 222; Conservative 0; Mismatches 0;
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Patent No. 6063988
GENERAL INFORMATION:
APPLICANT: Rudiger Hain, Regina Fischer
TITLE OF INVENTION: DNA SEQUENCE AND ITS USE
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS: ADDRESSE: SPRUNG KRAMER SCHAEFER & BRISCOE
STREET: 660 White Plains Road
                                                Sequence 4, Application US/09810861B
Patent No. 6770799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
                            JS-09-810-861B-4/C
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US-08-836-402B-7/c
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APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
TITLE OF INVENTION: DNA CONStruct Containing Bacillus
NUMBER OF SEGUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6229075artis Corporation
                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                  2.3%; Score 175; DB 3; Length 532;
99.3%; Pred. No. 7.9e-57;
tive 0; Mismatches 2; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: FILOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PILING DATE:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,426
FILING DATE: March 13, 1998
ATTORNEY/AGENT INFORMATION:
NAME: HOACL, Thomas
REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
TELECOMMUNICATION INFORMATION:
TELEPRAX: (919) 541-8614
TELEPRAX: (919) 541-8619
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-330-760-1/c
; Sequence 1, Application US/09330760
; Patent No. 6229075
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 512 base pairs
TYPE: nucleic acid
STRANDEDNES: double
STRANDEDNES: double
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
MANTI-SENSE: NO
IMMEDIATE SOURCE:
CONE: 35S Promoter
US-09-291-238-1
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Best Local Similarity 99.33
Matches 275; Conservative
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STATE: New Jersey
COUNTRY: USA
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Sequence 1, Application US/09291238
Patent No. 6222104
GENERAL INFORMATION:
APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6222104artis Corporation
                                                                                                                                                                                                                                                                                                                                                                                       .
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/291,238
FILING DATE:
                                                                                                                                                                                                                                                                                                                                        Score 175; DB 3;
Pred. No. 7.9e-57;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,426
FILING DATE: March 13, 1998
ATTORNEY/AGENT INFORMATION:
NAME: HOAVIE, THOMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
TELEPHONE: (919) S41-8614
TELEPHONE: (919) 541-8614
           TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 base pairs
TYPE: nucleic acid
STRANDEDNES: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 564 Morris Avenue
CITY: Summit
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                            Query Match 2.3%;
Best Local Similarity 99.3%;
Matches 275; Conservative (
                                                                                                                                                                                                                               ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: 35S Promoter
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US-09-291-238-1/c
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6250 IGTICCTCGTGGGGTGGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCATCTTGAACGA 6309
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18-09-30-30-737-1/c

18-09-30-30-737-1/c

18-09-30-737-1/c

18-09-30-70-70-1/c

18-09-30-70-70-1/c

18-
                                                                                                                                                                                                                                                                                                                                                                  Score 175; DB 3; Length 532;
Pred. No. 7.9e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6430 TITGITGAAAAGTCTCAATAGCCCTCTGGTCTTCTGA 6466
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/330,737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTTGTTGAAAGTCTCAATAGCCCTCTGGTCTTCTGA 13
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99.3%; Pred. No. /...
0; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/042,426
FILING DATE: March 13, 1998
ATTORNEY/ABENT INFORMATION:
NAME: HOxie, Thomas
REGISTRATION NUMBER: 32,993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: 358 Promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 13
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (919) 541-8614
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 564 Morris Avenue
CITY: Summit
STATE: New Jersey
COUNTRY: USA
LENGTH: 532 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 99.34
Matches 275; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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US-09-328-473-1
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5 Sequence 1, Application US/09328473

7 Patent No. 6232533

7 GENERAL INFORMATION:

APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi

7 TITLE OF INVENTION:

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 6232533artis Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                    2.3%; Score 175; DB 3; Length 532; 99.3%; Pred. No. 7.9e-57;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/328,473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49 TTTGTTGAAAGTCTCAATAGCCCTCTGGTCTTCTGA 13
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CLASSIFICATION
FILING APPLICATION
PRIOR APPLICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,426
FILING DATE: March 13, 1998
ATTORNEY/AGENT INFORMATION:
NAME: HOxie, Thomas
REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
TELECOMMUNICATION INFORMATION:
TELEPANE: (919) 541-8614
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                           LENGTH: 532 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: 355 Promoter
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 99.3
Matches 275, Conservative
      SEQUENCE CHARACTERISTICS
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6309

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TITCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCCCGGATATTACCC 6429
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Sequence 1, Application US/09330714A
Patent No. 6342660
GENERAL INFORMATION:
APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
TITLE OF INVENTION: DNA Construct Containing Bacillus
TITLE OF THVENTION: Thuringiensis Gene
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0
                                                                                                                                                                                                           Length 532;
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ADDRESSEE: No. 6342660artis Corporation
                                                                                                                                                                                                           Score 175; DB 3;
Pred. No. 7.9e-57;
0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/330,714A
FILING DATE: 11-Jun-1999
CLASSIFICATION: «UNKnown»
PRIOR APPLICATION DATA:
APPLICATION UNDBER: 09/042,426
FILING DATE: «UNKnown»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                        CLONE: 35S Promoter
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Hoxie, Thomas
REGISTRATION NUMBER: 32,993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 564 Morris Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
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               TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
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LENGTH: 532 base pairs
STRANDEDNESS: double
                                                                                                                                                                                                             2.3%;
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COMPUTER READABLE FORM:
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STATE: New Jersey
COUNTRY: USA
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Matches 275; Conservative
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                                                                                                        IMMEDIATE SOURCE:
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US-09-330-714A-1/c
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TITLE OF INVENTION: DNA Construct Containing Bacillus
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/329,169
FILING DATE: 09-Jun-1999
CLASSIFICATION: AUNKnown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,426
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                      Length 532
                                                                                                                                                                                                                                                             Indels
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STREET: 564 Morris Avenue
CITY: Summit
STATE: New Jersey
                                                                                                                                                                                                                   Score 175; DB 3;
Pred. No. 7.9e-57;
                                                                                                                                                                                                                                                               0; Mismatches
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Hoxie, Thomas
REGISTRATION NUMBER: 32,993
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (919) 541-8689
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Patent No. 6329575
GENERAL INFORMATION:
      TYPE: nucleic acid
STRANDEDNES: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
HYPOTHETICAL: NO
HYPOTHETICAL: CONDE: 35S Promoter
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                                                                                                                                                                                                                      Query Match
Best Local Similarity 99.3%;
Matches 275; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
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US-09-329-169-1/c
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6370 TTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCCCGATATTACCC 6429
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Sequence 1. Application US/09289170

Datent No. 6573438

GENERAL INFORMATION:
APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
TITLE OF INVENTION: DNA CONStruct Containing Bacillus
NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6573438artis Corporation
                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                               2.3%; Score 175; DB 3; Length 532;
99.3%; Pred. No. 7.9e-57;
tive 0; Mismatches 2; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/289,170
FILING DATE:
CLASSIPICATION:
PRIOR APPLICATION NUMBER: 09/042,426
FILING DATE: MARCH 13, 1998
ATPONEY/AGENT INFORMATION:
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                                        TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: 35S Promoter
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Hoxie, Thomas
REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8614
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                              Matches 275; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 07901
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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US-09-289-170-1/c
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TITLE OF INVENTION: DNA Construct Containing Bacillus
NUMBER OF SEQUENCES: 11
CORRESPONDENCE DESS:
ADDRESSEE: No. 6399860artis Corporation
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                                                                                                                                                                                                                                                   Length 532
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99.3%; Pred. No. 7.9e-57;
tive 0; Mismatches 2; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/328,826
FILING DATE: 09-Jun-1999
CLASSIFICATION ATMA:
APPLICATION NUMBER: US/09/042,426
FILING DATE: MARCH 13, 1998
ATTORNEY AGENT INFORMATION:
                                                                                                                              IMMEDIATE SOURCE:
CLONE: 35S Promoter
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
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CITY: Summit
STATE: New Jersey
COUNTRY: USA
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TELEFAX: (919) 541-8689
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                                           TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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Patent No. 6399860
GENERAL INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: double
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SEQUENCE CHARACTERISTICS
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Matches 275; Conservative
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109 TITCGAIGAAGIGACAGAIAGCIGGGCAAIGGAAICCGAGGAGGTITCCCGAIAITACCC 50
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
MATT-SENSE: NO
IMMEDIATE SOURCE:
CLONE: 35S Promoter
US-09-289-170-1
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Search completed: December 31, 2005, 19:14:53 Job time : 843 secs

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1: /cgn2_6/ptodatal/lpubpna/USO8_NEW PUB.seq:*
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3: /cgn2_6/ptodatal/lpubpna/USO7_NEW PUB.seq:*
4: /cgn2_6/ptodatal/lpubpna/DST_NEW PUB.seq:*
5: /cgn2_6/ptodatal/lpubpna/DST_NEW PUB.seq:*
6: /cgn2_6/ptodatal/lpubpna/USI1_NEW_PUB.seq:*
7: /cgn2_6/ptodatal/lpubpna/USI1_NEW_PUB.seq:*
8: /cgn2_6/ptodatal/lpubpna/USI1_NEW_PUB.seq:*
9: /cgn2_6/ptodatal/lpubpna/USI1_NEW_PUB.seq:*
9: /cgn2_6/ptodatal/lpubpna/USI1_NEW_PUB.seq:*
10: /cgn2_6/ptodatal/lpubpna/USI1_NEW_PUB.seq:*
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Compugen Ltd
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US-11-038-981A-5

US-11-038-981A-1

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US-11-038-981A-18

US-11-038-981A-25

US-11-038-981A-25

US-11-038-981A-25

US-11-038-981A-26

US-11-038-981A-27

US-11-038-981A-28

US-11-038-981A-28

US-11-038-981A-15

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                                                                                                                                                          4172979 seqs, 262114271 residues
          version -
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                                           nucleic search, using sw model
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Gapop 60.0°, Gapext 60.0
          GenCore (c) 1993
                                                            December 31, 2005,
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Maximum DB seq length: 2000000000
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US-10-986-501-81
US-11-071-651-11
US-11-071-651-11
US-11-038-981A-1
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US-10-995-561-56237
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US-10-750-185-24652
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ALIGNMENTS

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                                                                    APPLICATION MATERIAL Science GmbH
TITLE OF INVENTION: Constructs and methods for regulating gene expression FILE REFERENCE: 53262-20065.00
CURRENT APPLICATION NUMBER: US,10/508,263
CURRENT PILING DATE: 2004-09-20
NUMBER OF SEQ ID NOS: 126
SOFTWARE: Patentin Ver. 2.1
LENGTH: 11667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8757 GATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCCCGATATTACCCTTTG
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99.3%; Pred. No. 1.1e-27;
tive 0; Mismatches 1;
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US-11-038-981A-5/c
US-11-038-981A-5/c
; Sequence 5, Application US/11038981A
; Publication No. US20050283856A1
; GENERAL INFORMATION:
; APPLICANT: COnner, Timothy W.
; APPLICANT: Plasinski, Stanislaw
; APPLICANT: Pag, Sheng Z
Sequence 122, Application US/10508263 Publication No. US20050260754A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial sequence
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Matches 148; Conservative
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LENGTH: 835
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Publication No. US20050278799A1
GENERAL INFORMATION:
APPLICANT: SHINOZAKI, Kazuko
APPLICANT: SATSURA, Koji
APPLICANT: TITO, Yusuke
TITLE OF INVENTION: Stress Induced Promoter Derived From Rice
FILE REFERENCE: 382.1041
CURRENT APPLICATION NUMBER: US/10/391,414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/11038981A

Publication No. US20050283856A1

GENERAL INFORMATION:

APPLICANT: Conner, Timothy W.

APPLICANT: Plasinski, Stanislaw

APPLICANT: Pang, Sheng Z

APPLICANT: You, Jinsong

TITLE OF INVENTION: CHIMBERIC PROMOTERS FOR USE IN PLANTS

FILE REFERENCE: 38-21(51446)

CURRENT FILING DATE: 2005-01-20

PRIOR APPLICATION NUMBER: US/11/038,981A

PRIOR APPLICATION NUMBER: 60/537,793

PRIOR PLICATION NUMBER: 60/537,793

NUMBER OF SEQ ID NOS: 35
                                                                                                                                                                                                                                                                                           Query Match 0.8%; Score 62; DB 7; Length 332; Best Local Similarity 100.0%; Pred. No. 4.5e-14; Matches 62; Conservative 0; Mismatches 0; Indels
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APPLICANT: You, Jinsong
TITLE OF INVENTION: CHIMBRIC PROMOTERS FOR USE IN PLANTS
FILE REFERENCE: 38-21(51446)B
CURRENT APPLICATION NUMBER: US/11/038,981A
CURRENT FILING DATE: 2005-01-20
PRIOR PPLICATION NUMBER: 60/537,793
PRIOR FILING DATE: 2004-01-20
NUMBER OF SEQ ID NOS: 35
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                                                                                                                                                                                                            TYPE: DNA ORGANISM: Cauliflower mosaic virus
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US-10-391-414-10/c
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Sequence 18, Application US/11038981A
Publication No. US20050283856A1
GENERAL INFORMATION:
APPLICANT: Conner, Timothy W.
APPLICANT: Pang, Sheng Z
APPLICANT: Pang, Sheng Z
APPLICANT: Pang, Sheng Z
TITLE OF INVENTION: CHIMBRIC PROMOTERS FOR USE IN PLANTS
FILE REFERENCE: 38-21(51446) B
CURRENT APPLICATION NUMBER: 2005-01-20
PRIOR APPLICATION NUMBER: 60/537,793
PRIOR PILING DATE: 2004-01-20
NUMBER OF SEQ ID NOS: 35
SEQ ID NO 18
LENGTH: 1273
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Best Local Similarity 100.0%; Pred. No. 3.9e-14;
Matches 62; Conservative 0; Mismatches 0; Indels
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Publication No. US20050283856A1
GENERAL INFORMATION:
APPLICANT: Conner, Timothy W.
APPLICANT: Flasinski, Stanislaw
APPLICANT: Pang, Sheng Z
APPLICANT: You, Jinsong
TITLE OF INVENTION: CHIMBERIC PROMOTERS FOR USE IN PLANTS
FILE REPERENCH: 38-21 (51446)B
CURRENT APPLICATION NUMBER: US/11/038,981A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , OTHER INFORMATION: Artificial promoter sequence US-11-038-981A-18
                      2002-377316
                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Cauliflower mosaic virus
US-10-391-414-10
CURRENT FILING DATE: 2003-03-10;
PRIOR APPLICATION NUMBER: JP 200;
PRIOR FILING DATE: 2002-12-26
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
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US-11-038-981A-20/c
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Gaps

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Indels

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6190 AGATATCACATCAATCCACTTGCTTTGAAGACGTGGTTGGAACGTCTTTTTTCCACGA 6249
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                                                                                                                                                                                                                                                                                                   Length 1935;
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Sequence 26, Application US/11018981A

Publication No. USCO50283856A1

GENERAL INFORMATION:

APPLICANT: Conner, Timothy W.

APPLICANT: Plasinski, Stanislaw

APPLICANT: Pang, Sheng Z

APPLICANT: POU, Jinsong

TITLE OF INVENTION: CHIMERIC PROMOTERS FOR USE IN PLANTS

FILE REFERENCE: 38-21(51446)B

CURRENT APPLICATION NUMBER: US/11/038,981A

CURRENT FILING DATE: 2005-01-20

PRIOR PILING DATE: 2004-01-20

NUMBER OF SEQ ID NOS: 35

SEQ ID NOS: 35
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Publication No. US20050283856A1
GENERAL INFORMATION:
APPLICANT: Conner, Timothy W.
APPLICANT: Flasinski, Stanislaw
APPLICANT: Pang, Sheng Z
APPLICANT: Wou, Jinsong
TITLE OF INVENTION: CHIMERIC PROMOTERS FOR USE IN PLANTS
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3.7e-14;
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0.8%; Score 62; DB 7; Le
Best Local Similarity 100.0%; Pred. No. 3.7e-14;
Matches 62; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                             ; OTHER INFORMATION: Artificial promoter sequence
US-11-038-981A-25
                                                                                                                                                                                                                                                                                            Query Match 0.8%; Score 62; DB Best Local Similarity 100.0%; Pred. No. 3.7 Matches 62; Conservative 0; Mismatches
CURRENT APPLICATION NUMBER: US/11/038,981A CURRENT FILING DATE: 2005-01-20 PRIOR APPLICATION NUMBER: 60/537,793 PRIOR FILING DATE: 2004-01-20 NUMBER OF SEQ ID NOS: 35 LENGTH: 1935
                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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ORGANISM: Artificial Sequence
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US-11-038-981A-24/C
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Publication No. US20050283856A1

GENERAL INFORMATION:

APPLICANT: Conner, Timothy W.

APPLICANT: Flaatski, Stanislaw

APPLICANT: Pang, Sheng Z

APPLICANT: Pang, Sheng Z

PITLE OF INVENTION: GILMERIC PROMOTERS FOR USE IN PLANTS

FILE REFERENCE: 38-21(51446)B

CURRENT APPLICATION UNMER: 08/11/038,981A

CURRENT APPLICATION NUMBER: 6005-01-20

PRIOR FILING DATE: 2004-01-20

PRIOR FILING DATE: 2004-01-20

NUMBER OF SEQ ID NOS: 35

SEQ ID NO 19

LENGTH: 1281
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                                                                                                                                                                                                            OTHER INFORMATION: Artificial promoter sequence
  CURRENT FILING DATE: 2005-01-20
PRIOR APPLICATION NUMBER: 60/537,793
PRIOR FILING DATE: 2004-01-20
NUMBER OF EQ ID NOS: 35
SEQ ID NO 20
LENGTH: 1273
TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Matches 62; Conserv
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US-11-038-981A-25/c
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US-11-038-981A-19/c
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TITLE OF INVENTION: CHIMERIC PROMOTERS FOR USE IN PLANTS
                 FILE REFERENCE: 38-21(51446)B
CURRENT APPLICATION NUMBER: US/11/038,981A
CURRENT FILING DATE: 2005-01-20
PRIOR APPLICATION NUMBER: 60/537,793
PRIOR FILING DATE: 2004-01-20
NUMBER OF SEQ ID NOS: 35
SEQ ID NO 28
                                                                                                                                                                                                                                                                                                                                                                62; Conservative
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Best Local Similarity
Matches 62; Conserva
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US-11-192-801-23/c
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                                                                                                                                                                                                                                                                                                  0.8%; Score 62; DB 7; Length 1939; 100.0%; Pred. No. 3.7e-14; tive 0; Mismatches 0; Indels
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Sequence 27, Application US/11038981A

PUBLICATION NO. US20050283856A1

GENERAL INFORMATION:
APPLICANT: Flashiski, Stanislaw
APPLICANT: Flashiski, Stanislaw
APPLICANT: Flashiski, Stanislaw
APPLICANT: Pang, Sheng Z
APPLICANT: Pang, Jinsong
TITLE OP INVENTION: CHIMERIC PROMOTERS FOR USE IN PLANTS
FILE REFERENCE: 38-21(51446)B
CURRENT APPLICATION NUMBER: US/11/038,981A
CURRENT APPLICATION NUMBER: 60/537,793
PRIOR FILING DATE: 2005-01-20
PRIOR FILING DATE: 2004-01-20

NUMBER OF SEQ ID NOS: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) OTHER INFORMATION: Artificial promoter sequence US-11-038-981A-27
                                                                                                                                                                                                                            ; OTHER INFORMATION: Artificial promoter sequence US-11-038-981A-24
FILE REPERENCE: 38-21(51446)B
CURRENT APPLICATION NUMBER: US/11/038,981A
CURRENT FILING DATE: 2005-01-20
PRIOR APPLICATION NUMBER: 60/537,793
PRIOR FILING DATE: 2004-01-20
NUMBER OF SEQ ID NOS: 35
LENGTH: 1939
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Sequence 28, Application US/11038981A

Publication No. US20050283856A1

GENERAL INFORMATION:
APPLICANT: Conner, Timothy W.
APPLICANT: Plasingki, Stanislaw
APPLICANT: Pang, Sheng Z

APPLICANT: You, Jinsong
                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
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Matches 62; Conservative
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LENGTH: 1963
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Sequence 23, Application US/11192801

Publication No. US20050273882A1

GENERAL INFORMATION:

APPLICANT: Romano, Charles P.

TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants

FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1135 AGATATCACATCAATCCACTTGCTTTGAAGACGTGGAACGTCTTTTTTTCCACGA 1076
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Sequence 29, Application US/11038981A

Publication No. US20050283856A1

GENERAL INFORMATION:

APPLICANT: Conner, Timochy W.

APPLICANT: Plasinski, Stanislaw

APPLICANT: Pang, Sheng Z

APPLICANT: You, Jinsong

ITLE OF INVENTION: CHIMERIC PROMOTERS FOR USE IN PLANTS

FILE REPREMENCE: 38-21 (51446)B

CURRENT APPLICATION NUMBER: US/11/038,981A

CURRENT FILING DATE: 2005-01-20

PRIOR APPLICATION NUMBER: 60/537,793

PRIOR PILING DATE: 2004-01-20

NUMBER OF SEQ ID NOS: 35

SEQ ID NO 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1971;
                                                                                                                                        Length 1963;
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0.8%; Score 62; DB 7; Lk
Best Local Similarity 100.0%; Pred. No. 3.7e-14;
Matches 62; Conservative 0; Mismatches 0;
                                                                                                                                        Score 62; DB 7; La
Pred. No. 3.7e-14;
                                                               ) OTHER INFORMATION: Artificial promoter sequence US-11-038-981A-28
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TYPE: DNA ORGANISM: Artificial Sequence
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Search completed: December 31, 2005, 20:22:35
Job'time : 470 secs
  FEATURE:
NAME/KEY: promoter
LOCATION: (25)..(640)
OTHER INFORMATION: P-CAMV.35S
FEATURE:
NAME/KEY: intron
LOCATION: (669)..(1472)
OTHER INFORMATION: I-Zm.HBp70
                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: terminator
LOCATION: (3475)..(3
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Sequence 15, Application No. US20050273882A1

GENERAL INFORMATION:

APPLICANT: Romano, Charles P.

TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants

FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn

CURRENT APPLICATION NUMBER: US/11/192,801

CURRENT FILING DATE: 2005-07-29

PRIOR FILING DATE: 2002-08-29

PRIOR FILING DATE: 1999-08-19

NUMBER OF SEQ ID NOS: 43

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 15

LENGTH: 3754
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NAME/KEY: CDS
LOCATION: (1241)..(3199)
OTHER INFORMATION: Cry3Bbl variant 11231mv2
CURRENT APPLICATION NUMBER: US/11/192,801
CURRENT FILING DATE: 2005-07-29
PRIOR APPLICATION NUMBER: US/10/232,665
PRIOR FILING DATE: 2002-08-29
PRIOR PLILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SQOTHARE: Patentin Ver. 2.0
SEQ ID NO 23
LENGTH: 3469
                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: promoter
LOCATION: (25)..(640)
OTHER INFORMATION: P-CAWV.35S
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LOCATION: (3217).. (3450)
CTHER INFORMATION: T-Ta.hsp17
US-11-192-801-23
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ORGANISM: Artificial Sequence
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LOCATION: (664)..(734)
OTHER INFORMATION: L-Ta.hcbl
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NAME/KEY: intron
LOCATION: (748)..(1238)
OTHER INFORMATION: I-OS.Actl
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                                                                                                                                 LOCATION: (3475)..(3730)
OTHER INFORMATION: Agrobacterium tumefaciens nos 3' transcription
OTHER INFORMATION: termination and polyadenylation sequence
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NAME/KEY: CDS
LOCATION: (1490)..(3448)
OTHER INFORMATION: Cry3Bb1 variant v11231
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OO O OOOO OOOOOOOOOOOOOOOOOOOOOOOOOOOO		RESULT 1 CNSOGS OU LOCUS DEFINITION ACCESSION VERYOODS SOURCE ORGANISM TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL COMMENT COMMENT COMMENT
GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd. OM nucleic - nucleic search, using sw model Run on: December 31, 2005, 05:24:09; Search time 17827 Seconds (without alignments) 19893.761 Million cell updates/sec Title: US-10-650-249-1 Perfect score: 7580 Sequence: 1 agctctattaattcaagagagccgccaccgcggtggagct 7580 Scoring table: 0.1GGO_NUC Scoring table: 0.1GGO_NUC Searched: 41078325 seqs, 23393541228 residues Word size & 0 Total number of hits satisfying chosen parameters: 82156650	length: 0 length: 2000000000	Database EST:*

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/note="Wector: pDS-Lox; Sequence generated in the course of an Arabidopsis T-DNA tagging program. TAIL-PCR was used to generate sequencing templates that represent A.t. genomic DNA flanking the left boxder of the pDs-Lox T-DNA insert. PCR products were sequenced directly by using the p745 primer 5' AACGTCCGCAAIGTGTTAITAAGTTGTC 3'"
                                                                                                                                                                                                                                 CW802337 17-480J24 Arabidopsis thaliana T-DNA insertion flanking sequences Arabidopsis thaliana genomic, genomic survey sequence.
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transformants"
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Arabidopsis thaliana
Bukaryota;
Bukaryota;
Syermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 736)
Woody, S.T., Monson, S.S., Jester, P.J., Austin-Phillips, S.,
Amasino, R.M., Sussman, M.R., and Krysan, P.J.
A New Community Resource for Knocking-Out Small Genes and
Tandemly-Duplicated Gene Families and for Mosaic Analysis in
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100.0%; Pred. No. 0;
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University of Wisconsin-Madison
425 Henry Mall, Madison, WI 53706,
Tel: (608) 262-4640
Email: swood/@facstaff.wisc.edu
Class: TAIL-PCR.
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KEYWORDS
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DEFINITION
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/note="Vector: pDS-Lox; Sequence generated in the course of an Arabidopsis T-DNA tagging program. TAIL-FCR was used to generate sequencing templates that represent A.t. genomic DNA flanking the left border of the pDs-Lox T-DNA insert. PCR products were sequenced directly by using the p745 primer 5' AACGTCCGCAATGTGTTATTAAGTTGTC 3'"
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Arabidopsis thaliana Full-length CDNA Complete sequence from clone GSLTFB53ZB03 of Flowers and buds of strain col-0 of Arabidopsis Exaina (thale cress).

BX822618
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   /clone lib="Arabidopsis thaliana
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Arabidopsis thaliana
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Spermatophyta; Magnoliophyta; eudicotyledons;
Cosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases I to 720)
Woody, S.T., Monson, S.S., Jester, P.J., Austin-Phillips, S.,
Amasino, R.M., Sussman, M.R. and Krysan, P.J.
A New Community Resource for Knocking-Out Small Genes and
Tandemly-Duplicated Gene Families and for Mosaic Analysis in
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/mol_type="genomic DNA"
/cultivar="Col-O ecotype"
/db_xref="taxon:3702"
/tisue_type="seeds produced by r
transformants"
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Biotechnology Center
University of Wisconsin-Madison
Als Henry Mall, Madison, WI 53706,
Tel: (608) 262-4640
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Daraces, Costantino, Vittorioso, Davies, Gilmartin, Giraudat, Parcy, Sablowski, Coupland, Martin, Angenent, Baeumlein, Carbonero, Colombo, Tonelli, owski, Coupland, Martin, Angenent, Baeumlein, Carbonero, Colombo, Tonelli, Engstroem, Droege-Laser, Gatz, Kavanagh, Kushnir, Zabeau, Laux, Holdsworth, Ruberti, Smeekens, Somessich, Weisshaar, Traes Research
Universitaetsstrasse 25, D-33594 Bielefeld, Germany
Emali: bernd, weisshaardeni-bielefeld, Germany
Emali: bernd, weisshaardeni-bielefeld, Germany
Data analysis performed in the frame of REGULATORS (Exploiting
Inter-species conservation in promoter sequences to identify
regulators of reproductive development and physiological
performance), a Trilateral Co-Operation in Plant Genomics between
Spain (WCYT), France (GENOPLANTE) and Germany (GABI) coordinated by
G. Coupland (coupland-ad-mpiz-koelln, mpg.de). Authors: Vincent
Thareau (IBP-Orsay UMR8618 CNRS-UPS, thareau-ad-ibp.u-psud.fr) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DR749973 868 bp mRNA linear EST 19-JUL-2005 79-L025823-065-006-G10-SeLA MPIZ-ADIS-065d Arabidopsis thaliana cDNA clone 006-G10, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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REGIA, an EU project on functional genomics of transcription factors from Arabidopsis thaliana

Comp. Funct. Genomics 3 (2), 102-108 (2002)
GGATGCATGGAGAATACCTCCATCACAAGCACACCAGCAATTCCCTTTCTTGATCAACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                571 TTACTCAAACCCTAGCAAGTTTCATAGCTACGGTCAAATCCCGGAGTTTAATTCCAACTT
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The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen) members carried out full-length librairies construction : Temple G. Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.

URGV INRA : Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). S prime and 3 prime are assembled with Phrap.
                                  Sukaryota; Virializates, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Wisiplantae; Streptophyta; Eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicacee; Arabidopsis.

1 (bases 1 to 1371)
Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M. Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
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/tissue_type="Flowers and
/ecotype="Col-0"
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/db_xref="taxon:3702"
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/gene="At3g55370"
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than 90 percent identity was found. The sequences were also blasted against all TigReS introow, and matches longer than 30 bp with 35 percent identity are reported as 'intron found'. The remaining terms for Segnalaya's describe the outcome of the evaluation of the Cros describe the outcome of the evaluation of the Cros derected after pairwise alignment with CDS plus pseudogenes from the TigReS protein file: The sequences or contigs for which a full CDS detected after pairwise alignment with CDS plus pseudogenes faul CDS detected after pairwise languages are partial good. Detect of the sequence, post pairwise than 55 percent identity over less of the participants on proved to be difficult on the Residuation of the Conse condition of the Maisshaan', the plasmid on proved to be difficult of the Residuation of the Conse condition of the Maisshaan', the plasmid of conservation and th
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4352 4412 4233 TGGTGGAACGTGCTCGGATCGCAAAAGTCCCATTGCCTGAAGCAGCTCTAAATTGCCCTA 4292 CTGTTGGAGGAGGCTTTAGGAGGAACAAGAGAAGCAAATCCAGATCGAAATCTACGGTCG 4472 132 192 CTGTTGGAGGAGGCTTTAGGAGGAACAAGAGAAGCAAATCCAGATCGAAATCTACGGTCG 312 4293 GATGTGACTCAACCAATACTAAGTTCTGTTACTTCAATAACTATAGCCTTACTCAACCTC 133 GATGTGACTCAACCAATACTAAGTTCTGTTACTTCAATAACTATAGCCTTACTCAACCTC 193 GCCATTICTGCAAACATGTCGTCGCTATTGGACACGTGGCGGTTCCTTGAGGAATGTTC 73 regregaacerecearcecaarecearecearrecerraagementaarecera GCCATTTCTGCAAAACATGTCGTCGCTATTGGACACGTGGCGCTTCCTTGAGGAATGTTC 0; Gaps Length 868; 0; Indels Query Match 7.7%; Score 580; DB 8; Le Best Local Similarity 100.0%; Pred. No. 1.2e-258; Matches 580; Conservative 0; Mismatches 0; 4353 253 4413 ORIGIN 셤 셤 ઠે 셤 ઠે ð ઠે

473 TGGTCTCGACTGATAATACTACTAGTACTTCATCACTTACTT	4533 ACCCTAGGAAGITICAIAGCIACGGICAAAICCCGGAGITIAATICCAACTIGCCCAICT 4592 	593 IGCCTCCTCTCCAAGCCTTGGAGATTACAATTCAAGCAACACTGGATTAGATTTTGGTG 4652 	4653 GAACTCAAATAAGCAACATGATAAGTGGTATGAGTTCTAGTGGGTCGGATCTTGGATGCAT 4712 	4713 GGAGAATACCTCCATCACAAGCTCAGCAATTCCCTTTCTTGATCAACACTACCGGAT 4772 	773 TGGTGCAATCTTCAAACGCGTTATATCCATTACTAGAAGG 4812 	DRYSO042 DRYSO042 N 79-L021445-065-006-G10-SelB MPIZ-ADIS-065d Arabidopsis thaliana CDNA clone 006-G10, mRNA sequence. DRYSO042. I GI:71035382 BRYSO042. I GI:71035382 BRYSO042. I GI:71035382 RABIdOSPSIS thaliana (thale cress) Arabidopsis thaliana (thale cress) RABIDOSPSIS thaliana (thale cress) N Arabidopsis thaliana (thale cress) RABIDOSPSIS (Tridiplantes) Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicocylacons; core eudicocylacons; crosids; eurocopids (the season) of the season of the se	according to clones and clustered. If more than one contig was formed, the clone was designated 'Contamination', The contigs and
Oy Db	Qy 4 Db	Oy du	Qy GD	Qy 4 Db	Oy 4	RESULT 6 DR 750042/C LOCUS DEFINITION ACCESSION VERYWORDS SOURCE ORGANISM TITLE JOURNAL COMMENT	

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ORIGIN d ò ò 4292 4352 4412 4413 CTGTTGGAGGAGGCTTTAGGAGGAACAAGAGAAGCAAATCCAGATCGAAATCTACGGTCG 4472 496 768 GCCATITICIGCAAAACAIGICGICGCIAIIGGACACGIGGCGGIICCIIGAGGAAIGIIC 709 4233 TGGTGGAACGTGCTCGGATCGCAAAAGTCCCATTGCCTGAAGCAGCTCTAAATTGCCCTA GATGTGACTCAACCAATACTAAGTTCTGTTACTTCAATAACTATAGCCTTAACTCAACCTC GCCATTTCTGCAAACATGTCGTCGCTATTGGACACGTGGCGGTTCCTTGAGGAATGTTC regregaacerecereceareceaaaaerecearrecereaaeceeereaarrecera 0; Gaps 7.7%; Score 580; DB 8; Length 972; 00.0%; Pred. No. 1.2e-258; 0; Indels Query Match
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Best Local Similarity 100.0%; Pred. No. 1.2
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                                                                                                                                       ACCCTAGCAAGTTTCATAGCTACGGTCAAATCCCGGAGTTTAATTCCAACTTGCCCATCT 4592
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Submitted (25-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRA cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr |
Location/Qualifiers
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CIGITICAGAGGAGCTTTAGGAGGAACAAGAGAAACCAAATCCAGATCGAAATCTACGGTCG 649
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/mol_type="genomic DNA"
db_rrf="taxon:3702"
/clone="F9G12"
/clone lib="IGF"
/cctype="Columbia"
/note="end : I7"
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100.0%; Pred. No. 2.3e-234;
ive 0; Mismatches 0;
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Bielefeld University, Institute for Genome Research
Universitaetsstrasse 25, D-33594 Bielefeld, Germany
Email: bernd.weisshaarwenni-bielefeld.de
AGI: AT3G55370; SeqAmalysis: truncated in 5' at pos 179;
Translation: no full cds detected
Data analysis performed in the frame of REGULATORS (Exploiting inter-species conservation in promoter sequences to identify regulators of reproductive development and physiological performance), a Trilateral Co-Operation in Plant Genomics between Spain (MCYT), France (GENOPLANTE) and Germany (GABI) coordinated by G. Coupland-cad-mpiz-koeln.mpg.de). Authors: Vincent Thareau (IBP-Oresy UMR8618 CNRS-UPS, thareau-ad-lbp.u-psud.fr) and Alain Lecharny (URGV-Evry UMR INRA-CNRS-UBUE,
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REGIA, an BU project on functional genomics of transcription factors from Arabidopsis thaliana
Comp. Funct. Genomics 3 (2), 102-108 (2002)
ACTITICGGGATAAAAATCTCGCCATGCAAAGGTAATTITATITITICATGACAAAGCCA 120
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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79-L021444-065-006-G10-SeLA MPIZ-ADIS-065d Arabidopsis thaliana
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Arabidopsis thaliana (thale cress)
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lecharny-ad-ibp.u-psud.fr).

Definition of the terms used to describe the quality of the clone: The about 220 sequences from the clone collection were sorted according to clones and clustered. If more than one contig was formed, the clone was designated 'Contamination'. The contigs and singletcons were blasted against CDS plus pseudogenes from the TIGRYS annotation, and the resulting AGI code is presented if more than 90 percent identity was found. The sequences were also blasted against all TIGRYS introns, and matches longer than 50 bp with 95 percent identity are reported as 'intron found'. The remaining terms for SeqAnalysis describe the outcome of the evaluation of the CDS detected after pairwise alignment with CDS plus pseudogenes from the TIGRYS annotation file. The sequences or contigs for which a full CDS with or without STOP codon was detected, a BLASTP against all TIGRYS proceed sequences was performed. Full perfect: 100 percent identity, full good: better than 95 percent identity over less than 95 percent of the sequence; weak similarity: less than 95 percent of the sequence; weak similarity: less than 95 percent of the sequence; that the collection contains a few clones for which that the collection contains a few clones for which the the collection contains a few clones for which sequencing was
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Location/Qualifiers
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99.5%; Pred. No. 8.6e-180;
iive 0; Mismatches 3;
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/clone="006-G10"
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/ecotype="Columbia"
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Matches 561; Conservative
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B97814 11-MAR-1998 143 bp DNA linear GSS 31-MAR-1998 F18P18TFB IGF Arabidopsis thaliana genomic clone F18P18, genomic
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Rounaley,S.D., Field,C.E., Bass,S., Linher,K., Linher,K.,
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Adams,M.D. and
Venter,J.C.
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L Unpublished (1997)
Cother GSSS: F18P18TR
Cother GSS: F18P18TR
Cother GSS
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                                            5.3%; Score 403; DB 9; Le
100.0%; Pred. No. 4.9e-176;
ive 0; Mismatches 0;
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/organism="Arabidopsis thaliana"
/mol type="genomic DNA"
/ecotype="Columbia".
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/clone="F18P18"
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Vencer, J.C.

Use of a BAC End Sequence Database To Identify Minimal Overlaps for Arabidopsis Genomic Sequencing

L Unpublished (1997)

Contact: Steve Rounsley

Contact: Steve Rounsley

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9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0208

Fax: 301 838 0208

Email: rounsley@tigr.org

Seq primmer: Mi3-21

Class: BAC ends

High quality sequence stop: 486.
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/note="Vector: BeloBACII; Site_1: EcoRI; Site_2: EcoRI;
Produced by Thomas Altmann"
                                                                                                                                                                                                                                              274 TACTACTAGTACTTCATCACTTACTTCTCGCCCAAGTTACTCAAATTTTAGCAAGTTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   514 ACAACAAGCTCAGCAATTCCCTTTCTTGATCAACACTACCGGATTGGTGCAATCTTCAAA
                              154 AIGTCGTCGTCGTATTGGACACGTGGCGGTTCCTTGAGGAATGTTCCTGTTGGAGGAGGGGCTT
                                                                                                                                   214 TAGGAGGAACAAGAGAAGCAAATCCAGATCGAAATCTACGGTCGTGGTCTCGACTGATAA
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                                                                                                          TAGGAGGAACAAGAAGCAAATCCAGATCGAAATCTACGGTCGTGGTCTCGACTGATAA
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/organism="Arabidopsis thaliana"
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CK437874 linear EST 29-JUN-2005
GQ0042.BR_P12 GQ004: Non-lignified secondary xylem from mature
trees Picea glauca cDNA clone GenomeQuebec_Id:GQ0042P12 5', mRNA
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1 (bases 1 to 441)

Morency,M.-J., Cooke,J., Pavy,N., Parsons,L., Paule,C., Seguin,A., Retzel,E., Butterfield,Y., Barber,S., Yang,G., Stott,J., Atholt,R., Marra,M. and MacKay,J.

Arborea EST sequencing in Picea glauca (white spruce)
Unpublished (2004)
                                                                                                                                                                          /clone_lib="IGF"
/note="Vector: BeloBACII; Site_1: EcoRI; Site_2: EcoRI;
Produced by Thomas Altmann"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        GACTGATAATACTACTAGTACTTCATCATCATTACTTCTCGCCCAAGTTACTCAAACCCTAG
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Centre de Recherche en Biologie Forestiere
                                                                                                                                                                                                                                                                        4.9%; Score 369; DB 9; I 99.8%; Pred. No. 3.6e-160; ative 0; Mismatches 1;
                                                   /organism="Arabidopsis th
/mol_type="genomic DNA"
/eoctype="columbia"
/db_xref="taxon:3702"
/clone="F24E16"
High quality sequence stop: 452.
Location/Qualifiers
                                                                                                                                                       /sex="hermaphrodite"
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosida; eurosida II; Brassicales; Brassicaceae; Arabidopsis.

I (Dasses I to 452)
S Rounsley, S.D., Suh, E.J., Wible, C., Golden, K., Shatsman, S., Choi, P., Yu, K., Akinretoye, B., Shen, K., Goonasekaram, S., Militscher, J.,
Adams, M.D. and Venter, J.C.,
A BAC End Sequence Database for Identifying Minimal Overlaps in
Arabidopsis Genomic Sequencing. Update 4
Unpublished (1998)
Contact: Steve Rounsley
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Fax: 301 838 0208
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/sex="hermaphrodite"
/close_lib="IGF"
/note="Vector: BeloBAGII; Site_1: EcoRI; Site_2: EcoRI;
Produced by Thomas Altmann"
                                                                                                                                                                                                                                                                            5519 TATATTAAACGTACTTAAGTCGAATTTTATGACCAAAGTAAATTATGCCGAATGTA
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                                                                                                                  Length 433
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99.8%; Pred. No. 3.1e-166;
tive 0; Mismatches 1;
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Seg primer: M13-21
Class: BAC ends
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Fax: 517-353-9168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "note="Organ: Stem from ground to lower part of live crown, on 33 year old tree; Vector: pBluescript II SK (+) KR, Site_1: Eco-RI; Site_2: Xho-I; Tissue was harvested in mid-June, during formation of early wood. cDNA was prepared from 5 mg of poly A+ selected RNA and was diectionmally ligated into the pBluescript II SK (+) XR vector (Stratagene), transformed by electroporation into DH108 cells (In vitrogen) for propagation"
University of Minnesota, MN id Identifier: MNS176207 Clone ID: GQ0042 P12 Clones available through: John MacKay, Ph. D. Professeur adjoint -Assistant professor EMAIL: jmackay@rsvs.ulaval.ca Centre de Recherche en Biologie Forestiere (Forest Biology Research Center) Universite Laval Quebec, Quebec CANADA GIK 7P4 Plate: 2 row: 12 column: P Seq primer: M13 Reverse Primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="Non-lignified differentiating secondary xylem from normal vertical trees" | dev stage="Non-lignified secondary xylem from trees | dev stage="Non-lignified secondary xylem from trees | dev stage="Non-lignified secondary xylem from trees | dev stage="E. coli DH10B cells" | dev stage="E. coli DH10B cells" | dev stage="Coli DH10B cells" | dev stage="Col DH10B cells"
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28394 Lambda-PRL2 Arabidopsis thaliana cDNA clone 104F10XP 3', mRNA
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Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Agnoliophyta; eudicotyledons; core eudicotyledons;
                                                                                                                                                                                                                                                                                                               /organism="Picea glauca"
/mol_type="mRNA"
/strain="Two trees of provenance 5333 and one from 5206"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6370 TITCGAIGAAGIGACAGAIAGCIGGGCAAIGGAAICCGAGGAGGITICCCGAIAITACCC
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100.0%; Pred. No. 1e-138;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="GenomeQuebec_Id:GQ0042P12"
/sex="Hermaphrodite"
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Best Local Similarity 100.
Matches 323; Conservative
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rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 446)

Newman, T., deBruijn, F.J., Green, P., Keegstra, K., Kende, H.,

McIntosh, L., Ohirogge, J., Raikhel, N., Somerville, S., Thomashow, M.,

Retzel, E. and Somerville, C.

Genes galore: a summary of methods for accessing results from

large-scale partial sequencing of anonymous Arabidopsis cDNA clones

Plant Physiol. 106, 1241-1255 (1994)
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MSU-DOE-FRL, Michigan State University, Plant Biology Bldg., E.
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Pred. No. 2.2e-115; 
0; Mismatches 1; Indels
                                                                                                                                                                 7846151
Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
                                                                                                                                                                                                                                                                                                             Email: 22313tcr@ibm.cl.msu.edu
The sequence entry for this EST is being submitted in the sense (Seq primer: M13 -21 dye primer.
Location/Qualifiers
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AQ361936 AQ361936 GI:4211775
GSS.
Magnaporthe grisea (anamorph: Pyricularia grisea)
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                                                                                                Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe. . (bases 1 to 199)
Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R., Phillips, K., Sasinowski, M. Wing, R.A. and Dean, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                         Clemson University
100 Jordan Hall, Clemson University, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
Class: BAC ends
High quality sequence stop: 96.
                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Magnaporthe grisea"
/mol_type="genomic DNA"
/strain="70-15"
/db xref="taxon:148305"
/clone="mgxb0004F23f"
/tab hose="Re-"ercoplasts"
/clone="mg-"ercoplasts"
/clone="lib="cUGI Rice Blast BAC Library"
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                                                                   Magnaporthe grisea (anamorph: Pyricularia grisea)
Magnaporthe grisea
clone mgxb0004F23f, genomic survey sequence.
AQ361597.1 GI:4211436
                                                                                                                                                                                                                              Contact: Dean RA
Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6494 GACGAGAGTGTCGTGCTCCACCATGTTGG 6522
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                                                                                                                                                                                                                 Unpublished (1998)
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                                                                                  ORGANISM
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/u_xil="caxonilator" / /u_xil="caxonilator" / /u_xil="caxonilator" / /u_xil="caxonilator" / /u_xil="caxonilator" / /uo.note="voctor" /uo.note="voctor: pBACWICH; Site_1: HindIII; Site_2: HindIII; /note="voctor: pBACWICH; Site_1: HindIII; Site_2: HindIII; /note="voctor: pBACWICH; Site_1: HindIII; Site_2: HindIII; /note="voctor: pBACWICH; Site_1: HindIII; Site_2: HindIII; /note="voctor with a note of world wide. It is a filamentous ascomycete with a haploid genome (n=7) of approximately 40 Mbp. Rice blast is an important model fungal pathogen for studying numerous aspects of the fungal-host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25X genome coverage. High density colony filters are available upon request."
                                                                                                          1 (bases 1 to 492)
Yu, Y., Zhu, H., Boyd,C.A., Gaudette,B., Gayle,A., Kingsbury,R.,
Phillips,K., Sasinowski,M. Wing,R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
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                                        Sordariomycetes;
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Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
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Clemson University Genomics Institute
Clemson University
Clemson University
Clemson University
Clemson University
Clemson Hall, Clemson University, Clemson, SC 29634
Tel: 864 656 4293
Email: rdean@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
Class: BAC ende
High quality sequence stop: 75.
Location/Qualifiers
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Best Local Similarity 99.3%; Pred. No. 9.9e-34;
Matches 148; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Magnaporthe grisea"
/mol_type="genomic DNA"
/strain="70-15"
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                                                                                                                                                                                                                                                                                   Unpublished (1998)
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Sequence Sequence Sequence

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ALIGNMENTS

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Sequence 1, Application US/10650249
Publication No. US20040045055A1
Publication No. US20040045055A1
GENERAL INFORMATION:
APPLICANT: Neff, Michael M
TITLE OF INVENTION: THE GENE FOR A DOF TRANSCRIPTION FACTOR CAPABLE OF ALTERING
TITLE OF INVENTION: THE SIZE AND STATURE OF A PLANT
FILE REPERRINCE: WSHU 2064.1
CURRENT APPLICATION NUMBER: US/10/650,249
PRIOR RILING DATE: 2003-08-02
PRIOR PILING DATE: 2002-08-02
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100.0%; Pred. No. 0;
ive 0; Mismatches
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
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Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                     GATATICITGGAGTAGACGAGAGTGTCGTGCTCCACCATGTTGGGGGATCTAGATATCACA
                                                                                                                        TCAATCCACTTGCTTTGAAGACGTGGTTGGAACGTCTTCTTTTCCACGATGTTCCTCGT
                                                                                                                                           1000 TCAATCCACTTGCTTTGAAGACGTGGTTGGAACGTCTTCTTTTTCCACGATGTTCCTCGT
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                                                                                     TTGAACGATAGCCTTTCCTTTATCGCAATGACGCATTTTGTAGAAGCCATCTTTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Wagner, Ry
APPLICANT: Wathews, Helena
APPLICANT: Mathews, Helena
APPLICANT: Liu, Xing Liang
APPLICANT: Waggoner, Wency J.
TITLE OF INVENTION: TRAIT-ASSOCIATED GENE IDENTIFICATION
TITLE OF INVENTION: METHOD
TITLE REPERENCE: 4257-0018:30
CURRENT APPLICATION NUMBER: US/09/522,334
CURRENT PILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: US 60/124,232
PRIOR PILING DATE: 1999-03-12
NUMBER OF SEQ ID NOSS: 28
SOFTWARE: FastSEQ for Windows Version 4.0
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US-09-522-334-1/c
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Sequence 20. Application US/10650249
Sequence 20. Application US/20040045055A1
Fublication No. US20040045055A1
GENERAL INFORMATION:
APPLICANT: Neff, Michael M
TITLE OF INVENTION: THE GENE FOR A DOF TRANSCRIPTION PACTOR CAPABLE OF ALTERING
TITLE OF INVENTION: THE SIZE AND STATURE OF A PLANT
TITLE OF INVENTION: THE SIZE AND STATURE OF A PLANT
FILE REFERENCE: WSHU 2064.1
CURRENT APPLICATION NUMBER: US/0650,249
CURRENT FILING DATE: 2003-08-28
FRIOR APPLICATION NUMBER: US 60/406,657
PRIOR FILING DATE: 2002-08-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 20
INSURTY

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14.0%; Score 1062; E
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1062; Conservative 0; Mismatches
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US-10-650-249-20
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                                                                                                 Sequence 17, Application US/10650249
Publication No. US20040045055A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: THE GIRE FOR A DOF TRANSCRIPTION FACTOR CAPABLE OF ALTERING TITLE OF INVENTION: THE SIZE AND STATURE OP A PLANT TITLE OF INVENTION: THE SIZE AND STATURE OP A PLANT TITLE OF INVENTION: THE SIZE AND STATURE OP A PLANT CURRENT APPLICATION NUMBER: US/10/650,249
CURRENT FILING DATE: 2003-08-28
PRIOR APPLICATION NUMBER: US 60/406,657
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
SEQ ID NOS: 20
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          40 ATTCTTGGAGTAGACGAGAGTGTCGTGCTCCACCATGTTG 1
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                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Arabidopsis thaliana
                                                                                               US-10-650-249-17
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| Sequence 15, Application US/10650249
| Sequence 15, Application Wo. US20040045055A1
| Publication No. US20040045055A1
| General INFORMATION:
| APPLICANT: Neff, Michael M
| TITLE OF INVENTION: THE GENE FOR A DOF TRANSCRIPTION FACTOR CAPABLE OF ALTERING
| TITLE OF INVENTION: THE SIZE AND STATURE OF A PLANT
| FILE REFERENCE: WSHU 2064.1
| FURRENT PELING DATE: 2003-08-28
| PRIOR FILING DATE: 2003-08-28
| PRIOR FILING DATE: 2003-08-28
| NUMBER OF SEQ ID NOS: 20
| SOFTWARE: Patentin version 3.1
| SEQ ID NO 15
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                 TTGGTGCAATCTTCAAACGCGTTATATCCATTACTAGAAGGTAAGGGAGGTGTTAATCAA
                                                                                                                                                                                                              GATITITICITCAGGCGGGGTTAGCGCCACGCAAAAAAAATGTGAAGGCGGAAGAGAAT
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9.0%; Score 684; DB 7; Length 684;
Best Local Similarity 100.0%; Pred. No. 1.3e-298;
Matches 684; Conservative 0; Mismatches 0; Indels
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US-10-650-249-15
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Publication No. US20040045055A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: THE GENE FOR A DOF TRANSCRIPTION FACTOR CAPABLE OF ALTERING
TITLE OF INVENTION: THE SIZE AND STATURE OF A PLANT
TITLE OF INVENTION: THE SIZE AND STATURE OF A PLANT
TITLE OF INVENTION: THE SIZE AND STATURE OF A PLANT
TITLE OF INVENTION: USHURER: US/10/650,249
CURRENT APPLICATION NUMBER: US/10/650,249
CURRENT FILING DATE: 2003-08-02
RIOR FILING DATE: 2003-08-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PARENT IN VERSION 3.1
SEQ ID NOS: 20
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                                                     3945 TGAAAAACTATAATTAATCTGCAATTCTTGTCAAAGTAGTCACAATTTTTATCTATTTTC
                                                                         901 TGAAAAACTATAAATCTGCAATTCTTGTCAAAGTAGTAGTCACAATTTTTATCTATTTTC
841 GTTTAAAGTTACTATGACTTTAATCTGAGTTATTATCCATTTTTTGCAGCTTTGT
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                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-650-249-12
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Best Local Similarity 100.0
Matches 888; Conservative
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US-10-650-249-12
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GENERAL INFORMATION:

APPLICANT: Mendel Biotechnology, Inc.
APPLICANT: RATCLIFFE, Oliver
APPLICANT: RATCLIFFE, Oliver
APPLICANT: RECEMBAN, Jose Luis
APPLICANT: RECEMBAN, Jose Luis
APPLICANT: ADAM, Luc J
APPLICANT: BICHARN, Jacqueline E
APPLICANT: PIGATH, Marsha L
APPLICANT: PIGATH, Marsha L
APPLICANT: RUBER, T Lynne
APPLICANT: RUBER, T Lynne
APPLICANT: RUBER, T Lynne
APPLICANT: RUBER, Robert A
APPLICANT: RUBER, Robert A
APPLICANT: RUBER, Robert A
APPLICANT: RUBER, Robert A
APPLICANT: BROUN, Pierre E
TITLE OF INVANTION' Yield-Related Polynucleotides and Polypeptides in Plants
APPLICANT: BROUN, Pierre E
TITLE OF INVANTION' Yield-Related Polynucleotides and Polypeptides in Plants
APPLICANT: BROUN, Pierre E
TITLE OF INVANTION' VIELD-80-99
PRIOR RUBER PELICATION NUMBER: 09/837, 444
PRIOR FILING DATE: 2001-04-18
PRIOR PELICATION NUMBER: 60/316, 049
PRIOR PELICATION NUMBER: 60/316, 049
PRIOR PELICATION NUMBER: 60/316, 049
PRIOR FILING DATE: 2001-12-05
PRIOR PELICATION NUMBER: 10/171, 468
PRIOR FILING DATE: 2001-12-05

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Sequence 7187, Application US/10487901

Sequence 7187, Application No. US20050091708A1

GENERAL INFORMATION:
APPLICANT: Oreido, Jeremia Vincent
APPLICANT: Miller, Barbara
APPLICANT: Miller, Barbara
APPLICANT: Miller, Barbara
APPLICANT: Blakeslee, Beth
APPLICANT: Blakeslee, Beth
APPLICANT: Blakeslee, Beth
APPLICANT: Shukla, Vipula
APPLICANT: Crosley, Rodney
TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Characteri
FILE REFERENCE: DOW-08552

CURRENT APPLICANT: 2004-02-26
NUMBER OF SEQ ID NOS: 7560

SOFTWARE: PatentIn version 3.1

SEQ ID NO 7187

LENGTH: 645
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241 AGTGGTATGAGTTCTAGTGGTGGATCTTGGATGCATGGAGAATACCTCCATCACAACAA 300
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                                                                                     301 GCTCAGCAATTCCCTTTCTTGATCAACACTACCGGATTGGTGCAATCTTCAAACGCGTTA
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RESULT 13
US-10-225-066A-409
Sequence 409, Application US/10225066A
Publication No. US20050160493A9
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                                                                                                                                                                                                                                                                                                                         TIGCCTCCTCTCCAAAGCCTTGGAGATTACAATTCAAGCAACACTGGATTTAGATTTTGGT
                                                                                                         61 AGATGTGACTCAACCAATACTAAGTTCTGTTACTTCAATAACTAAGCTTACTCAACCT
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                                             4232 ATGGTGGAACGTGCTCGGATCGCAAAAGTCCCATTGCCTGAAGCAGCTCTAAATTGCCCT
                                                                 1 Argerggaacgrecregarcecaaaagrecearrecereaagcagercraaarrecer
                                                                                         4292 AGATGTGACTCAACCAATACTAAGTTCTGTTACTTCAATAACTATAGCCTTACTCAACCT
                                                                                                                                     CGCCATTTCTGCAAACATGTCGTCGCTATTGGACACGTGGCGGTTCCTTGAGGAATGTT
                                                                                                                                                                                   CCTGTTGGAGGAGGCTTTAGGAGGAACAAGAAGCAAATCCAGATCGAAATCTACGGTC
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Length 795;
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Best Local Similarity 100.0%; Pred. No. 5.8e-252;
Matches 581; Conservative 0; Mismatches 0; Indels
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US-10-374-780A-2767
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7.7%; Score 581; DB 7; Le
Best Local Similarity 100.0%; Pred. No. 5.8e-252;
Matches 581; Conservative 0; Mismatches 0;
PRIOR APPLICATION NUMBER: 09/934,455
PRIOR FILING DATE: 2001-08-22
PRIOR PILING DATE: 2001-08-22
PRIOR PILING DATE: 2001-11-19
PRIOR FILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: 60/336,692
PRIOR FILING DATE: 2001-12-11
PRIOR PILING DATE: 2002-06-14
PRIOR FILING DATE: 2002-06-09
PRIOR FILING DATE: 2002-08-09
PRIOR PILING DATE: 2002-08-09
PRIOR FILING DATE: 2002-08-09
PRIOR PILING DATE: 2002-08-09
NUMBER OF SEQ ID NOS: 2906
                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Arabidopsis thaliana
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US-10-374-780A-2767
                                                                                                                                                                                                                                                                                                                 SEQ ID NO 2767
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CAAAGGCTAATTTTGAGGCTCAAAGGAAAGGTATGGTTATAAAACTATCTTTTTGATCTT 5285
GTACATTGGTGCTTGTCATGCGAGTTATTGCTGAGGAAGATCAAACCATGCAGCTATATC 300
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                                                                                                               541 Tricgricciaricricaaaccccritarariccarracradaacc 581
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APPLICANT: Hoffman, Neil
APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: Chaliana
FILE REPERENCE: 2025US (PARA-014PRV)
CURRENT APPLICATION NUMBER: US/09/770,152
CURRENT APPLICATION NUMBER: 60/178,503
PRIOR FILING DATE: 2000-01-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 7.6%; Score 577; DB 3; L. Best Local Similarity 100.0%; Pred. No. 3.7e-250; Matches 577; Conservative 0; Mismatches 0;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 196
                                                                                                                                                                                                                        Sequence 196, Application US/09770152
Publication No. US20020040489A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matthew, Abraham V.
Ledford, Brooke L.
Woessner, Jeffrey P.
Haas, William David
                                                                                                                                                                                                                                                                                                                 An, Yong-Qiang
Hamilton, Carol M.
Price, Jennifer L.
Raines, Tracy M.
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Rameaka, Joshua G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Garcia, Carlos A.
Kricker, Maja
Slader, Ted
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Allen, Keith
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US-09-770-152-196
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                                                                               APPLICANT: ALEMAN, Luc J
APPLICANT: ALEMAN, Luc J
APPLICANT: DUBELL, Arnold T
APPLICANT: HERBL, Jacqueline E
APPLICANT: HERBL, Jacqueline E
APPLICANT: HERBL, Jacqueline E
APPLICANT: HERBL, Jacqueline E
APPLICANT: PIGERIM, Marcha L
APPLICANT: REGIMAN, Robert A
APPLICANT: REGIMAN, Robert A
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APPLICANT: PINEDA, Omaira
APPLICANT: PINEDA, Omaira
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FILE REFERENCE: MBI0036-2 US
CURRENT FILING DATE: 2001-04-18
FRIOR FILING DATE: 2001-04-18
FRIOR FILING DATE: 2001-04-08
FRIOR PELICATION NUMBER: 60/336,049
FRIOR PELICATION NUMBER: 60/338,692
FRIOR FILING DATE: 2001-12-05
FRIOR FILING DATE: 2001-12-11
FRIOR FILING DATE: 2002-06-14
NUMBER: PATCHING DATE: 2002-06-14
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                      Mendel Biotechnology,
RATCLIFFE, Oliver
RIECHMANN, Jose Luis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , окGANISM: Arabidopsis thaliana
US-10-225-066A-409
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LENGTH: 795
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APPLICANT: Wang, Xun

APPLICANT: WANGER: US/09/938, 842A

CURRENT APPLICATION NUMBER: US 60/227, 866

PRIOR PLING DATE: 2001-08-24

PRIOR PLING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/264, 647

PRIOR APPLICATION NUMBER: US 60/300,111

PRIOR PLING DATE: 2001-01-16

PRIOR PLING DATE: 2001-06-22

NUMBER 0F SEQ ID NOS: 5379

LENGTH: 2000
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                                                                                                                                              CAAGAGTTGATGTTGGAAACTTTTTTGTGTTCATTGAATAATCATCGAATTCTCAATT 5465
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301 CAAAGGCTAATTTTGAGGCTCAAAGGAAAGGTATGGTTATAAAACTATCTTTTGATCTT 360
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                                                                                                                                                                                                          5466 TCTTGGAGACCCATTATGAGACATTGAGACATCTATA 5502
                                                                                                                                                                                                                          541 TCTTGGAGACCCATTATGAGACATTGAGACATCTATA 577
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Best Local Similarity 100.0%; Pred. No. 1.9e-155;
Matches 368; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-3563
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US-09-938-842A-3563
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